

BEST AVAILABLE COPY

Access DB#

111840

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Maureen Wallenhorst Examiner #: 70465 Date: 1-12-04
 Art Unit: 1743 Phone Number 301-717-1266 Serial Number: 10/045,170
 Mail Box and Bldg/Room Location: Room 801 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Acid-Labile Isotope-Coded Extractant (ALICE) & Its Use
in Quantitative mass Spectrometric Analysis of Protein mixtures
 Inventors (please provide full names):

Yongchang Qiu, Jack H. Wang, Rodney M. Hewick

Earliest Priority Filing Date: Oct. 22, 2000

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for compound having a thiol -
 specific reactive group attached to a non-
 biological polymer via a linker - specifically,
 the compounds recited in claims 20, 12 & 13

Non-biological polymer can be polystyrene or
 polyethylene glycol

See highlighted areas on claims.

Thanks!

(Closest art is printed out first; don't panic, not that many actual abstracts here.)

STAFF USE ONLY

Searcher: EG
 Searcher Phone #: _____
 Searcher Location: _____
 Date Searcher Picked Up: _____
 Date Completed: 1-15-04
 Searcher Prep & Review Time: (5)
 Clerical Prep Time: _____
 Online Time: 1:10

Type of Search

NA Sequence (#) _____
 AA Sequence (#) _____
 Structure (#) (5)
 Bibliographic (1)
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN: 1497.56
 Dialog _____
 Questel/Orbit _____
 Dr.Link _____
 Lexis/Nexis _____
 Sequence Systems _____
 WWW/Internet _____
 Other (specify) _____

=> file reg

FILE 'REGISTRY' ENTERED AT 12:36:39 ON 13 JAN 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 American Chemical Society (ACS)

=> display history full ll-

L1 FILE 'LCA' ENTERED AT 09:39:10 ON 13 JAN 2004
19434 SEA (DETECT? OR SENSE# OR SENSING# OR ANALY? OR ANAL# OR
ASSAY? OR EST# OR ESTN# OR ESTIMAT? OR QUANTIF? OR
QUANTITAT? OR CALCULAT? OR CALC# OR CALCN# OR MEASUR? OR
MONITOR?)/BI,AB
L2 3688 SEA (DETECTOR? OR COUNTER? OR SENSOR? OR SPECTROG? OR
SPECTROMET? OR PYROMET? OR METER# OR METRE# OR GAUGE? OR
INDICATOR? OR RECORDER? OR ANALYZER? OR SCANNER? OR
COMPARATOR? OR INSPECTOR? OR MONITOR?)/BI,AB
L3 19714 SEA (DETERMIN? OR DETERMN# OR DET# OR DETN# OR EVALUAT?
OR ASCERTAIN? OR RECOGNI? OR IDENTIF? OR INDICAT? OR
DISTINGUISH? OR TEST OR TESTS OR TESTED OR TESTING# OR
DIAGNOS?)/BI,AB

L4 FILE 'HCA' ENTERED AT 09:47:38 ON 13 JAN 2004
208483 SEA (L1 OR L2 OR L3) (2A) PROTEIN?
L5 475295 SEA PEPTIDE# OR DIPEPTIDE# OR TRIPEPTIDE# OR TETRAPEPTIDE
OR PENTAPEPTIDE# OR POLYPEPTIDE#
L6 102329 SEA ?DISULFID? OR ?DISULPHID?
L7 3921 SEA (BLOCK? OR ENDCAP? OR CAP OR CAPS OR CAPPED OR
CAPPING# OR TERMINAT?) (2A) (REAG!NT? OR REACTANT? OR
COMPOUND# OR CMPD# OR CPD#)
L8 211541 SEA DIGEST?
L9 535848 SEA ISOTOP? OR RADIOISOTOP? OR RADIOLABEL? OR RADIOACTIV?
OR RADIO? (2A) (TAG OR TAGS OR TAGGED OR TAGGING# OR
LABEL? OR MARK? OR PROBE# OR PROBING#)

L10 FILE 'REGISTRY' ENTERED AT 09:52:13 ON 13 JAN 2004
E DEUTERIUM/CN
1 SEA DEUTERIUM/CN
L11 119947 SEA D/ELS

L12 FILE 'HCA' ENTERED AT 09:52:54 ON 13 JAN 2004
145585 SEA L10 OR DEUTERAT? OR DEUTERIUM# OR D2
L13 122458 SEA L11
L14 361209 SEA HPLCMS OR MS OR M(W)S OR MASS## (2A) SPEC?

FILE 'LREGISTRY' ENTERED AT 09:55:05 ON 13 JAN 2004

L15 STR

FILE 'REGISTRY' ENTERED AT 10:38:01 ON 13 JAN 2004
E CYSTEINE/CN

L16 2 SEA CYSTEINE/CN

FILE 'HCA' ENTERED AT 10:39:47 ON 13 JAN 2004

L17 105507 SEA L16 OR ?CYSTEINE?

L18 319 SEA L4 AND L5 AND (L6 OR SS OR S(W)S) AND L17

L19 0 SEA L18 AND L7

L20 65 SEA L18 AND L8

L21 22 SEA L18 AND L9

L22 72 SEA L18 AND L14

L23 5 SEA L18 AND (L12 OR L13)

D L23 1-5 AU

SEL L23 2,3 RN

FILE 'REGISTRY' ENTERED AT 10:47:28 ON 13 JAN 2004

L24 53 SEA (435314-09-3/BI OR 435314-15-1/BI OR 435314-17-3/BI

L25 2 SEA L24 AND L11

L26 1 SEA 436144-22-8/BI

FILE 'HCA' ENTERED AT 11:01:26 ON 13 JAN 2004

L27 1 SEA L26

L28 10 SEA L20 AND L21

L29 29 SEA L20 AND L22

L30 7 SEA L21 AND L22

FILE 'REGISTRY' ENTERED AT 11:04:55 ON 13 JAN 2004

L31 114427 SEA L11 AND C/ELS

FILE 'HCA' ENTERED AT 11:06:55 ON 13 JAN 2004

L32 54928 SEA L31

L33 128 SEA L4 AND L32

FILE 'REGISTRY' ENTERED AT 11:08:29 ON 13 JAN 2004

E POLYSTYRENE/CN

L34 1 SEA POLYSTYRENE/CN

ACT EOEGPOPG/A

L35 (9682)SEA 75-21-8/CRN

L36 (21863)SEA 107-21-1/CRN

L37 (9283)SEA 75-56-9/CRN

L38 (8413)SEA 57-55-6/CRN

L39 (7690)SEA (L35 OR L36) AND (L37 OR L38)

L40 11 SEA L39 AND 2/NC

L41 FILE 'HCA' ENTERED AT 11:09:25 ON 13 JAN 2004
330322 SEA L34 OR POLYSTYRENE# OR STYRENE#

L42 FILE 'LCA' ENTERED AT 11:09:39 ON 13 JAN 2004
320 SEA (POLYGLYCOL# OR (POLYALKYLENE# OR POLYETHYLENE# OR
POLYPROPYLENE# OR POLYBUTYLENE# OR POLYISOBUTYLENE#) (2A) (GLYCOL# OR OXIDE#) OR (ETHYLENE# OR PROPYLENE# OR BUTYLENE# OR ISOBUTYLENE#) (2A) (POLYOXIDE# OR POLY(W)OXIDE#)) /BI,AB

L43 166 SEA (POLYOXYALKYLENE# OR POLYOXYETHYLENE# OR POLYOXYPROPYLENE# OR POLYOXYBUTYLENE# OR POLYOXYISOBUTYLENE# OR POLY(W) (GLYCOL# OR OXYALKYLENE# OR OXYETHYLENE# OR OXYPROPYLENE# OR OXYBUTYLENE# OR OXYISOBUTYLENE#)) /BI,AB

L44 63 SEA (POLYOXY(W) (ALKYLENE# OR ETHYLENE# OR PROPYLENE# OR BUTYLENE# OR ISOBUTYLENE#) OR PEG OR PPG OR PBG OR ALCOX# OR BREOX# OR CARBOWAX# OR EMKAPOL# OR LUTROL# OR MACROGOL# OR PEO OR PLURACOL# OR PLURIOL# OR POLIKOL# OR POLYOX#) /BI,AB

L45 7 SEA (SUPEROX# OR TENZILIN# OR ADEKA# OR ARCOL# OR EXCENOL# OR LAPROL# OR NIAX# OR PROPYLAN# OR SANNIX# OR VORANOL#) /BI,AB

L46 FILE 'HCA' ENTERED AT 11:14:17 ON 13 JAN 2004
216258 SEA L40 OR PEG OR L42 OR L43 OR L44 OR L45
L47 2 SEA L33 AND L41
L48 19 SEA L33 AND L46
L49 19 SEA L48 AND ((L5 OR L6 OR L7 OR L8 OR L9) OR L12 OR L13 OR L32 OR L14 OR L17)
L50 10 SEA L28 AND (L20 OR L21 OR L22)
L51 5 SEA L29 AND L21

L52 FILE 'REGISTRY' ENTERED AT 11:25:03 ON 13 JAN 2004
STR
L53 50 SEA SSS SAM L52
E 2508.150.23/RID
L54 16305 SEA 2508.150.23/RID
L55 49 SEA L54 AND L11

L56 FILE 'HCA' ENTERED AT 11:30:01 ON 13 JAN 2004
8278 SEA L54
L57 38 SEA L55
L58 1 SEA L57 AND L4
L59 1 SEA L57 AND ?PROTEIN?
L60 44 SEA L56 AND L4
L61 5 SEA L60 AND (L6 OR L17)
L62 21 SEA L60 AND (L5 OR L7 OR L8 OR L9 OR L12 OR L32 OR L14 OR L41 OR L46)

L63 15 SEA L62 AND L5
L64 0 SEA L62 AND L7
L65 3 SEA L62 AND L8
L66 4 SEA L62 AND L9
L67 2 SEA L62 AND L12
L68 1 SEA L62 AND L32
L69 6 SEA L60 AND L14
L70 2 SEA L60 AND L41
L71 3 SEA L60 AND L46
L72 11 SEA (L65 OR L66 OR L67 OR L68 OR L69 OR L70 OR L71)
L73 1 SEA L63 AND (L20 OR L21 OR L22 OR L29 OR L49)

FILE 'REGISTRY' ENTERED AT 11:45:12 ON 13 JAN 2004

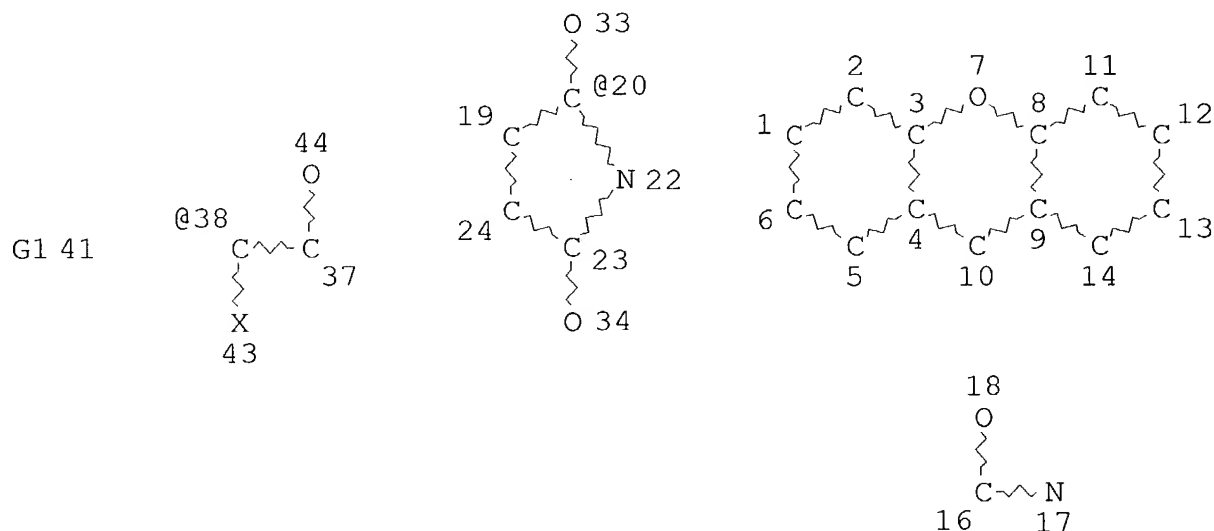
L74 10 SEA SSS SAM L15
L75 STR L15
L76 23 SEA SSS SAM L75
L77 421 SEA SSS FUL L75
SAV L77 WAL170/A

FILE 'HCA' ENTERED AT 11:52:07 ON 13 JAN 2004

L78 197 SEA L77
L79 87 SEA L78 AND ?PROTEIN?
L80 21 SEA L79 AND L4
L81 48 SEA L79 AND L5
L82 18 SEA L79 AND (L6 OR L17)
L83 0 SEA L79 AND L7
L84 3 SEA L79 AND L8
L85 8 SEA L79 AND L9
L86 1 SEA L79 AND (L12 OR L32)
L87 5 SEA L79 AND L14
L88 13 SEA L79 AND L17
L89 2 SEA L79 AND L41
L90 3 SEA L79 AND L46
L91 1 SEA L79 AND L57
L92 14 SEA L84 OR L85 OR L86 OR L87 OR L89 OR L90 OR L91
L93 12 SEA L80 AND L81
L94 7 SEA L80 AND L82
L95 14 SEA L81 AND L82
L96 18 SEA L23 OR L27 OR L30 OR L47 OR L51 OR L58 OR L59 OR L61
OR L73 OR L94
L97 10 SEA L92 NOT L96
L98 28 SEA L96 OR L92
L99 28 SEA (L28 OR L50 OR L72 OR L88 OR L93 OR L95) NOT L98
L100 52 SEA (L21 OR L29 OR L49) NOT (L98 OR L99)
L101 28 SEA (L21 OR L49) NOT (L98 OR L99)
L102 24 SEA L29 NOT (L98 OR L99 OR L101)

FILE 'REGISTRY' ENTERED AT 12:36:39 ON 13 JAN 2004

=> d 177 que stat
L75 STR



VAR G1=38/20

NODE ATTRIBUTES:

DEFAULT MLEVEL IS ATOM

DEFAULT ECLEVEL IS LIMITED

GRAPH ATTRIBUTES:

RING(S) ARE ISOLATED OR EMBEDDED

NUMBER OF NODES IS 29

STEREO ATTRIBUTES: NONE

L77 421 SEA FILE=REGISTRY SSS FUL L75

100.0% PROCESSED 6384 ITERATIONS

421 ANSWERS

SEARCH TIME: 00.00.01

=> file hca

FILE 'HCA' ENTERED AT 12:37:17 ON 13 JAN 2004

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

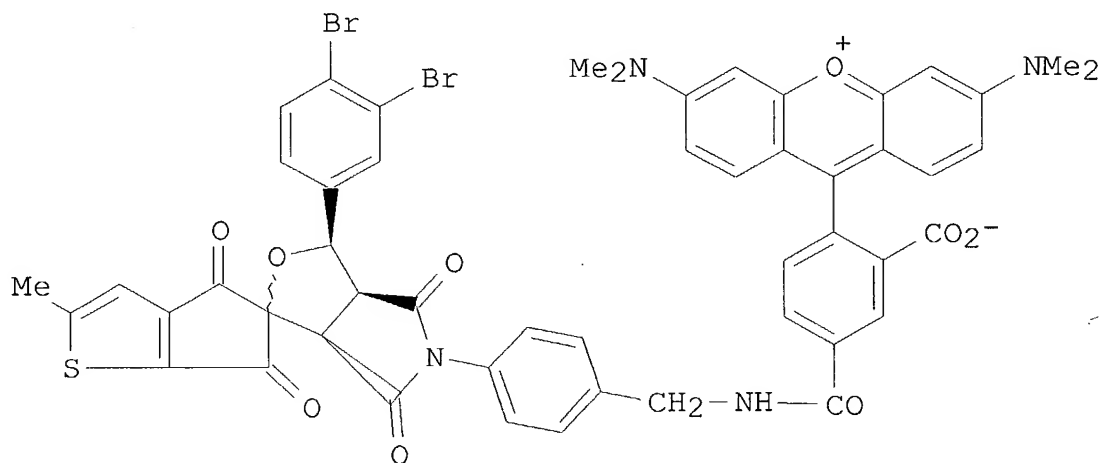
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

=> d 198 1-28 cbib abs hitstr hitind

L98 ANSWER 1 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:191379 E2 displacement assay for identifying inhibitors of human papillomavirus (HPV). White, Peter; Yoakim, Christiane (Boehringer Ingelheim (Canada) Ltd., Can.). PCT Int. Appl. WO 2003067259 A1 20030814, 56 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-CA155 20030204. PRIORITY: US 2002-PV355711 20020207.

GI



AB The invention provides an assay for identifying inhibitors of HPV, comprising: (a) contacting a HPV E2 transactivation domain with a probe to form a E2:probe complex and measuring a signal from the probe to establish a baseline level; (b) incubating the E2:probe complex with a test compd. and measuring the signal from the probe; (c) comparing the signal from step (b) with the signal from step (a). The probe is a heterocyclic spiro compd. (Markush included) or a deriv. thereof, wherein the deriv. includes a detectable label or an affinity tag. The signal is selected from fluorescence, resonance energy transfer, time-resolved fluorescence, **radioactivity**, fluorescence polarization, change in the intrinsic spectral properties, luminescence, and plasma-resonance. A modulation in the signal is an indication that the test compd.

binds to the transactivation domain. Prepn. of probe mols., e.g. I, is described.

IT 579487-93-7

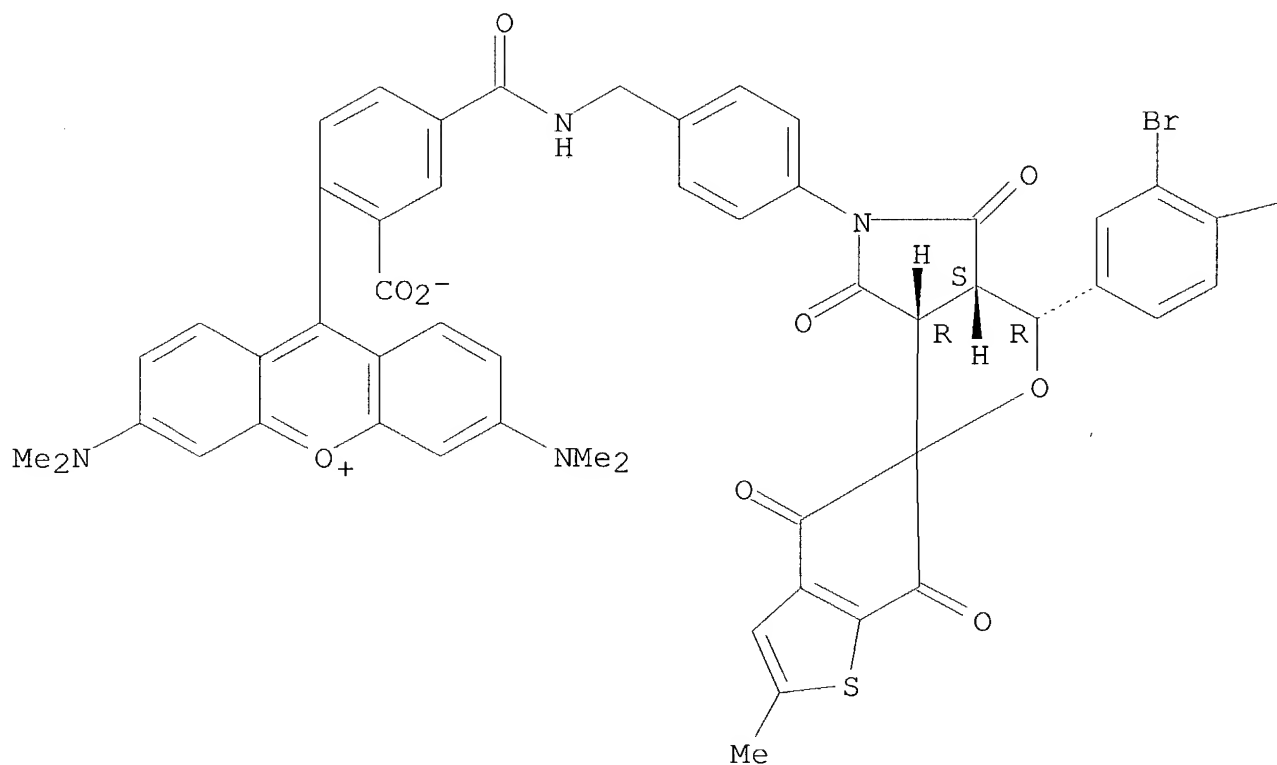
(E2 displacement assay for identifying inhibitors of HPV)

RN 579487-93-7 HCA

CN Xanthylum, 9-[2-carboxy-4-[[[4-[(3'R,3'aS,6'aR)-3'-(3,4-dibromophenyl)-3'a,4,4',6,6',6'a-hexahydro-2-methyl-4,4',6,6'-tetraoxospiro[5H-cyclopenta[b]thiophene-5,1'-[1H]furo[3,4-c]pyrrol]-5'(3'H)-yl]phenyl)methyl]amino]carbonyl]phenyl]-3,6-bis(dimethylamino)-, inner salt, rel- (9CI) (CA INDEX NAME)

Relative stereochemistry.

PAGE 1-A



PAGE 1-B

—Br

IC ICM G01N033-569
ICS C07D497-10
CC 1-5 (Pharmacology)
Section cross-reference(s): 28
IT Antiviral agents
Chemiluminescent substances
Colored materials
Drug screening
Epitopes
Human
Human papillomavirus
Human papillomavirus 11
Human papillomavirus 6
Protein sequences
Test kits
(E2 displacement assay for identifying inhibitors of HPV)
IT Proteins
(gene E1; E2 displacement assay for identifying inhibitors of HPV)
IT Proteins
(gene E2; E2 displacement assay for identifying inhibitors of HPV)
IT 58-85-5, Biotin 81-88-9 2321-07-5, Fluorescein 7440-53-1, Europium, biological studies 9014-00-0, Luciferase 10028-17-8, Tritium, biological studies 14158-31-7, Iodine-125, biological studies 14762-75-5, Carbon-14, biological studies 70281-37-7, Tetramethylrhodamine 82354-19-6, Texas red 121207-31-6, Bodipy 493/503 165599-63-3, Bodipy FL 579487-93-7 579487-94-8 579487-95-9 579487-96-0 579487-97-1 579487-98-2 579487-99-3 579488-00-9 579488-01-0 579488-02-1
(E2 displacement assay for identifying inhibitors of HPV)
IT 581976-50-3
(unclaimed protein sequence; e2 displacement assay for identifying inhibitors of human papillomavirus (HPV))

L98 ANSWER 2 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:97654 Lysine labeling reagent and methods of use. Peters, Eric C.;

Brock, Ansgar; Ericson, Christer (IRM LLC, Bermuda). PCT Int. Appl. WO 2003056299 A2 20030710, 63 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-US35581 20021105. PRIORITY: US 2001-PV332988 20011105; US 2002-PV385835 20020603; US 2002-PV410382 20020912.

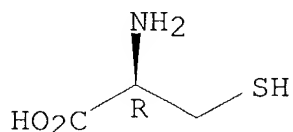
AB The present invention provides compds. which are useful as multifunctional labels in proteomics studies. The labels of the present invention are both lysine-specific and increase the overall sequence coverage obtained in **polypeptide** mapping expts., by for example, increasing the ionization efficiencies of lysine-terminated tryptic fragments. In certain aspects, the labels of the present invention can be used to measure differential quantitation, as for example, **deuterium(s)** can easily be introduced during their synthesis. In one aspect, a C-terminal derivatized lysine biases the fragment ion intensities strongly toward C-terminal fragment ions, resulting in a highly simplified tandem **mass spectrum**. In further aspects, the no. of lysine residues can be detd. in a **polypeptide**. 2-Methoxy-4,5-dihydro-1H-imidazole and 2-methoxy-4,5-tetradeutero-1H-imidazole were prepd. and used to label the lysine residues in myoglobin. The myoglobin was **digested** with trypsin and the **peptides** were analyzed by MALDI **mass spectrometry**.

IT 52-90-4, L-Cysteine, reactions
(labeling reagent for, for sequential labeling of **polypeptides**; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.

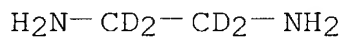


IT 37164-19-5, 1,2-Ethane-1,1,2,2-d4-diamine

(lysine-contg. **peptide** labeling reagent and use in
proteomics and **mass spectrometry**)

RN 37164-19-5 HCA

CN 1,2-Ethane-1,1,2,2-d4-diamine (9CI) (CA INDEX NAME)

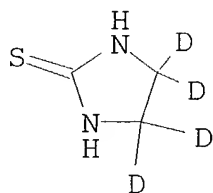


IT 352431-28-8P, 2-Imidazolidinethione-4,4,5,5-d4
557064-36-5P

(lysine-contg. **peptide** labeling reagent and use in
proteomics and **mass spectrometry**)

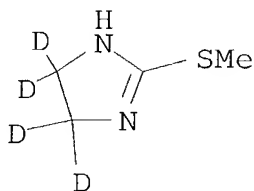
RN 352431-28-8 HCA

CN 2-Imidazolidinethione-4,4,5,5-d4 (9CI) (CA INDEX NAME)



RN 557064-36-5 HCA

CN 1H-Imidazole-4,5-d2, 4,5-dihydro-4,5-d2-2-(methylthio)-,
monohydriodide (9CI) (CA INDEX NAME)



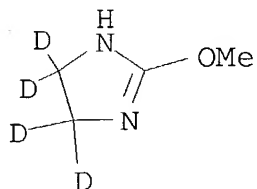
● HI

IT 402788-68-5P

(lysine-contg. **peptide** labeling reagent and use in
proteomics and **mass spectrometry**)

RN 402788-68-5 HCA

CN 1H-Imidazole-4,5-d2, 4,5-dihydro-4,5-d2-2-methoxy- (9CI) (CA INDEX
NAME)



- IT 7782-39-0, Deuterium, properties
(lysine-labeling reagent contg.; lysine-contg. **peptide**
labeling reagent and use in proteomics and **mass**
spectrometry)
- RN 7782-39-0 HCA
- CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)
- D-D
- IC ICM G01N
- CC 9-14 (Biochemical Methods)
Section cross-reference(s): 27
- ST lysine residue labeling reagent proteomics; **mass**
spectrometry labeled lysine **peptide**;
methoxyimidazole lysine labeling; **deuterium**
methoxyimidazole lysine labeling
- IT Ion cyclotron resonance **mass spectrometry**
(Fourier transform; lysine-contg. **peptide** labeling
reagent and use in proteomics and **mass**
spectrometry)
- IT Alcohols, reactions
(as carboxylic acid-labeling reagent for sequential labeling of
polypeptides; lysine-contg. **peptide** labeling
reagent and use in proteomics and **mass**
spectrometry)
- IT Composition
(detn. of no. of lysine residues in proteins; lysine-contg.
peptide labeling reagent and use in proteomics and
mass spectrometry)
- IT Enzymes, uses
(**digesting proteins**, in anal. of
derivatized **proteins** by **mass**
spectroscopy; lysine-contg. **peptide** labeling
reagent and use in proteomics and **mass**
spectrometry)
- IT Ionization
(efficiency of modified lysine-contg. **polypeptides**;
lysine-contg. **peptide** labeling reagent and use in

- proteomics and mass spectrometry)
- IT **Isotopes**
(in differential quantitation of lysine-contg. polypeptides; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Reagents**
(labeling lysine residues; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Myoglobins**
(labeling of lysine residues in and anal. of; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Carboxylic acids, reactions**
(labeling reagent for, for sequential labeling of polypeptides; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Electrospray ionization mass spectrometry**
Mass spectrometry
Protein sequences
(lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Peptides, biological studies**
Proteins
(lysine-contg.; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Proteins**
(modified, at lysine residues; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Esterification**
(of carboxylic acids in sequential labeling of polypeptides; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Laser ionization mass spectrometry**
(photodesorption, matrix-assisted; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Laser desorption mass spectrometry**
(photoionization, matrix-assisted; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)
- IT **Proteome**
(studies; lysine-contg. peptide labeling reagent and use in proteomics and mass spectrometry)

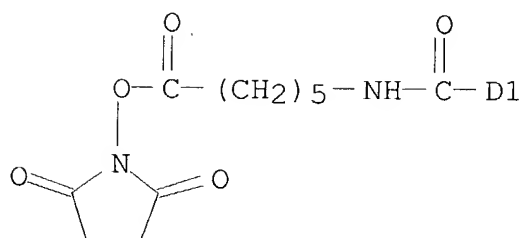
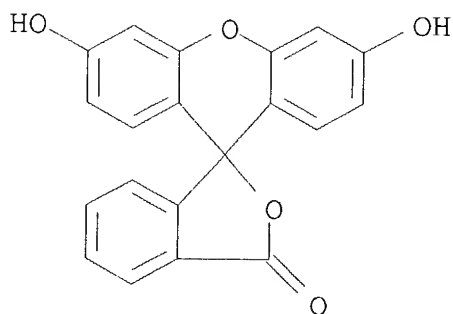
- IT Affinity
(tags; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 14464-29-0, Acetic acid N-hydroxysuccinimide ester
(N-termini of tryptic **peptides** labeling with; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 78348-28-4
(N-terminus of **peptide** labeling by; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 60108-34-1 299899-45-9 431063-78-4 543706-56-5 557064-37-6
557064-38-7 557064-39-8 557064-40-1 557064-41-2 557064-42-3
557064-43-4 557064-44-5 557064-45-6 557064-46-7 557064-47-8
557064-48-9 557064-49-0 557064-50-3
(amino acid sequence of tryptic **peptides** of horse myoglobin, derivatization and MALDI **mass spectrometry** in relation to; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 83404-43-7 106021-96-9 115918-58-6 145224-99-3
(amino acid sequence, **mass spectrometry** after lysine labeling of; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 71977-09-8
(amino acid sequence, sequential site-selective labeling of; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 52-90-4, L-Cysteine, reactions 74-79-3, L-Arginine, reactions
(labeling reagent for, for sequential labeling of **polypeptides**; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 557064-51-4
(lysine residue of **peptide** labeling by; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 56-87-1, L-Lysine, reactions
(lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 74-88-4, Iodomethane, reactions 75-15-0, Carbon **disulfide**, reactions 37164-19-5, 1,2-Ethane-1,1,2,2-d4-diamine 40322-87-0, 2-Methylthio-2-imidazoline hydroiodide
(lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 352431-28-8P, 2-Imidazolidinethione-4,4,5,5-d4

- 557064-36-5P
(lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 402788-68-5P
(lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 7782-39-0, Deuterium, properties
(lysine-labeling reagent contg.; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 9002-07-7, Trypsin
(lysine-modified myoglobin **digestion** with; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- IT 28118-54-9P
(**polypeptides** labeling with; lysine-contg. **peptide** labeling reagent and use in proteomics and **mass spectrometry**)
- L98 ANSWER 3 OF 28 HCA COPYRIGHT 2004 ACS on STN
138:381146 Methods for the detection, analysis and isolation of nascent **proteins** by labeling with reporter dyes using an aminoacyl-tRNA charged with a dye-conjugated amino acid. Rothschild, Kenneth J.; Gite, Sadanand; Olejnik, Jerzy (Ambergen, Inc., USA). U.S. Pat. Appl. Publ. US 2003092031 A1 20030515, 76 pp., Cont.-in-part of U.S. Ser. No. 49,332. (English). CODEN: USXXCO. APPLICATION: US 2002-174368 20020618. PRIORITY: US 1999-382736 19990825; WO 2000-US23233 20000823; US 2002-49332 20020621.
- AB A non-**radioactive** method of detection and anal. of nascent **proteins** translated within cellular or cell-free translation systems by labeling the nascent **protein** with a reporter dye is described. The core method involves charging a tRNA with an amino acid conjugated with a powerful fluorescent, preferably a deriv. of BODIPY (4,4-difluoro-4-bora-3a,4a-diaza-s-indacene). Alternatively, **protein** synthesis can be monitored by incorporating a dye-binding peptide into a **protein**. Binding of the dye to the **protein**, with a change in its spectral properties, can be used to monitor **protein** synthesis. Nascent **proteins** contg. these markers can be rapidly and efficiently detected, isolated and analyzed without the handling and disposal problems assocd. with **radioactive** reagents. Chem. synthesis of misaminoacylated tRNA-Lys by partial degrdn. of the 3'-end and resynthesis is demonstrated. The amino acid was also labeled with a photolabile biotin that allowed rapid recovery of the **protein** from cell-free translation with immobilized streptavidin. Lower limits of detection were in the range 0.3-10 ng **protein**.

IT 114616-31-8D, amino acid conjugates 527687-02-1D,
 amino acid conjugates
 (incorporation into nascent **proteins** of; methods for
 detection, anal. and isolation of nascent **proteins** by
 labeling with reporter dyes using aminoacyl-tRNA charged with
 dye-conjugated amino acid)

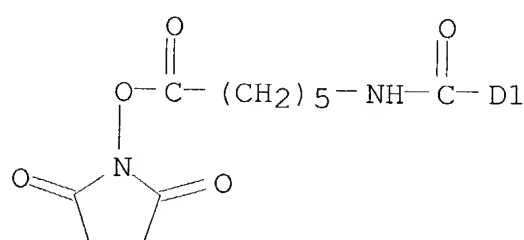
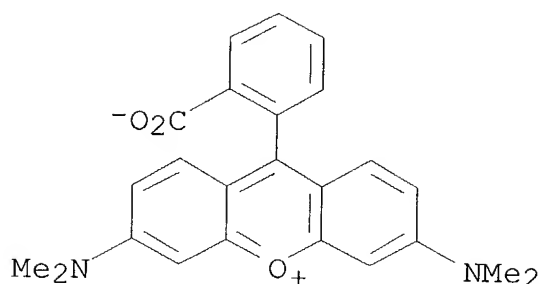
RN 114616-31-8 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-ar-carboxamide,
 N-[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]-3',6'-dihydroxy-3-
 oxo- (9CI) (CA INDEX NAME)



RN 527687-02-1 HCA

CN Xanthylium, 9-[2-carboxy-4(or 5)-[[[6-[(2,5-dioxo-1-
 pyrrolidinyl)oxy]-6-oxohexyl]amino]carbonyl]phenyl]-3,6-
 bis(dimethylamino)-, inner salt (9CI) (CA INDEX NAME)



- IC C12Q001-68; C12P019-34
 NCL 435006000
 CC 6-1 (General Biochemistry)
 Section cross-reference(s): 3, 9
 ST **protein** nascent detection fluorescent dye incorporation
 tRNA misaminoacylation
 IT tRNA
 (aminoacyl, dye-labeled; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
 IT Bacteriorhodopsins
 (apobacteriorhodopsins, detection of synthesis of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
 IT **Proteins**
 (carbohydrate-binding, detection of synthesis of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
 IT Translation, genetic
 (cell-free, detection of nascent **proteins** in; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
 IT Translation, genetic
 (detection of nascent **proteins** in; methods for

detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)

- IT Antigens
- Cytokines
- Enzymes, analysis
- Fusion **proteins** (chimeric **proteins**)
- Hormones, animal, analysis
 - (detection of synthesis of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Escherichia coli
 - (exts., labeling of nascent **proteins** in; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Fluorometry
 - (for detection of dye-labeling of nascent **proteins**; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Wheat
 - (germ, exts., labeling of nascent **proteins** in; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Avidins
 - (in purifn. of nascent **proteins** labeled with biotin derivs.; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT tRNA
 - (initiator, labeling by misaminoacylation of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT tRNA
 - (labeling by misaminoacylation of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT **Proteins**
 - (lipid-binding, detection of synthesis of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Animal cell
- Pancreas

- Reticulocyte
(lysates, **protein** synthesis in, detection of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT tRNA
(lysine-specific, labeling by misaminoacylation of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT **Proteins**
(nucleic acid-binding, detection of synthesis of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Egg
(oocyte, **protein** synthesis in, detection of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Animal tissue culture
Insecta
(**protein** synthesis in, detection of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Bacteria (Eubacteria)
Human
Parasite
Virus
(**proteins** of, detection of synthesis of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT Hemolysins
(.alpha.-, detection of synthesis of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 524698-42-8
(detection in nascent **proteins** of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 37353-39-2, RNA ligase
(in prepn. misaminoacylated tRNA; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated

- amino acid)
- IT 75-77-4, Trimethylsilyl chloride, reactions
(in protection of deoxycytidine; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 9013-20-1, Streptavidin
(in purifn. of nascent **proteins** labeled with biotin derivs.; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 58-85-5D, Biotin, amino acid conjugates
(in purifn. of nascent **proteins**; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 2321-07-5D, Fluorescein, amino acid conjugates 16322-19-3D, amino acid conjugates 113721-87-2D, amino acid conjugates 114616-31-8D, amino acid conjugates 117548-22-8D, amino acid conjugates 145195-58-0D, amino acid conjugates 146616-66-2D, BODIPY-FL-SE, amino acid conjugates 155862-95-6D, amino acid conjugates 217190-15-3D, amino acid conjugates 217190-17-5D, BODIPY-FL-SSE, amino acid conjugates 303190-88-7D, amino acid conjugates 335193-70-9D, BODIPY-R6G-SE, amino acid conjugates 527687-02-1D, amino acid conjugates
(incorporation into nascent **proteins** of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 56-87-1D, L-Lysine, dye conjugates 63-68-3D, L-Methionine, dye conjugates
(incorporation into **proteins** of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 138026-71-8D, BODIPY, derivs., amino acid conjugates 165599-63-3D, BODIPY-FL, amino acid conjugates
(methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 9001-78-9, Alkaline phosphatase
(partial RNA cleavage with, for misaminoacylation; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 13444-71-8, Periodic acid
(partial RNA cleavage with, for misaminoacylation; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with

- dye-conjugated amino acid)
- IT 17776-78-2
(phosphorylation of deoxyribonucleotides using; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 133852-21-8P
(prepn. and reactions of, in prepn. misaminoacylated tRNAs; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 208660-68-8P 328387-23-1P 524698-40-6P
(prepn. and reactions of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 87424-19-9P
(prepn. and use in tRNA modification of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 951-77-9, Deoxycytidine
(protection and deprotection of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 69304-37-6
(reactions of in protection of adenosine; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 2592-95-2, 1-Hydroxybenzotriazole 56602-33-6, Benzotriazol-1-yloxy tris-(dimethylamino)phosphonium hexafluoro phosphate
(reactions of, in charging tRNA with coumarin amini acids; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 80817-46-5
(reactions of, in prepn. dinucleotides; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 60-32-2, 6-Aminocaproic acid 121-44-8, Triethylamine, reactions 1068-90-2, Diethylacetamidomalonate 6851-99-6, 2-Bromo,2'-nitroacetophenone 35013-72-0 35231-44-8, 4-(Bromomethyl)-7-methoxy coumarin 82911-69-1 524698-41-7
(reactions of; methods for detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using aminoacyl-tRNA charged with dye-conjugated amino acid)
- IT 526229-19-6 526229-20-9 526229-21-0 526229-22-1 526229-23-2

526229-24-3 526363-81-5

(unclaimed nucleotide sequence; methods for the detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using an aminoacyl-tRNA charged with a dye-conjugated amino acid)

IT 64134-30-1 92000-76-5 145646-22-6 205938-74-5

(unclaimed sequence; methods for the detection, anal. and isolation of nascent **proteins** by labeling with reporter dyes using an aminoacyl-tRNA charged with a dye-conjugated amino acid)

L98 ANSWER 4 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:164365 Can nuclear localization signals enhance nuclear localization of plasmid DNA?. Nagasaki, Takeshi; Myohoji, Teruhiko; Tachibana, Taro; Futaki, Shiroh; Tamagaki, Seizo (Department of Applied and Bioapplied Chemistry, Graduate School of Engineering, Osaka City University, Osaka, 558-8585, Japan). Bioconjugate Chemistry, 14(2), 282-286 (English) 2003. CODEN: BCCHEs. ISSN: 1043-1802. Publisher: American Chemical Society.

AB Nonviral vectors are safer and more cost-effective than viral vectors but are significantly less efficient, and thus, increasing the efficiency of nonviral vectors remains an important objective. One way to overcome this problem is by stimulating the nuclear localization of exogenous genes. Nuclear localization signals (NLSs) are known to be involved in the active transport of exogenous **proteins** and probes into the nucleus. However, stimulation of nuclear localization of plasmid DNA has yet to be confirmed completely. In the present study, we prepd. plasmid DNA-NLS peptide conjugates and adjusted spacer length and no. introduced in an attempt to increase transfection efficiency. In comparison to conjugates with unmodified plasmid DNA and short spacers, we found that NLS-plasmid DNA conjugates with covalent bonding by diazo coupling through PEG chain (MW 3400) stimulated complexation with the nuclear transport **proteins** importin .alpha. and importin .beta.. Evaluation of transfection showed higher expression efficiency with plasmid DNA-NLS peptide conjugates than with unmodified plasmids. However, evaluation of intracellular trafficking after microinjection into the cytoplasm showed plasmid DNA-NLS peptide conjugates only within the cytoplasm; there was no NLS-plasmid stimulation of nuclear localization. Our findings suggest that stimulation of plasmid nuclear localization cannot be achieved merely by changing spacer length or chem. modifying plasmid DNA-NLS peptide conjugates. An addnl. mechanism must be involved.

IT 486397-36-8DP, conjugated to plasmid pGL3 or pGFP

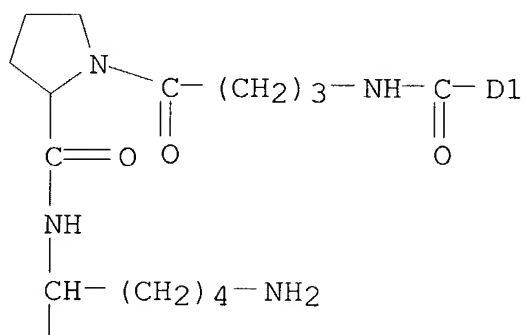
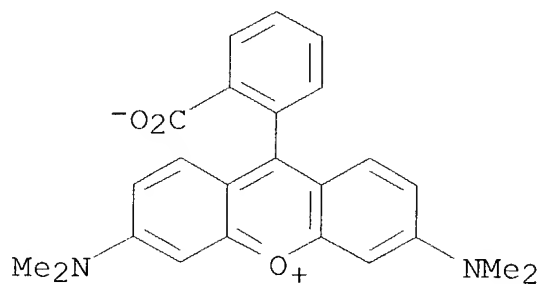
(evaluation of nuclear localization of plasmid DNA-nuclear localization signal peptide conjugate)

RN 486397-36-8 HCA

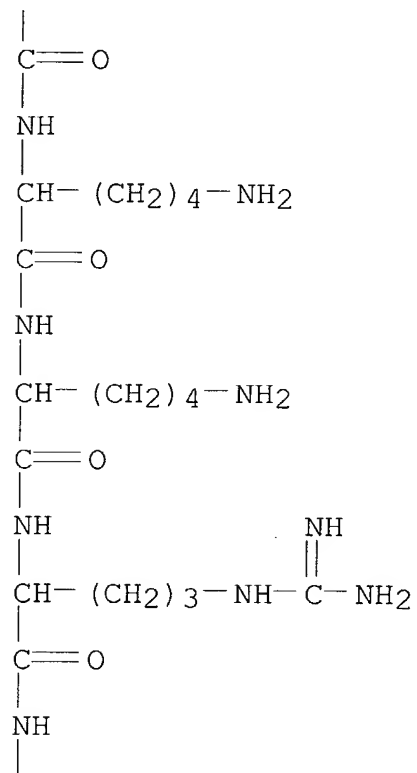
CN L-Cysteinamide, 1-[4-[[3(or 4)-[3,6-bis(dimethylamino)xanthylum-9-

yl]-4(or 3)-carboxybenzoyl]amino]-1-oxobutyl]-L-prolyl-L-lysyl-L-lysyl-L-lysyl-L-arginyl-L-lysyl-L-valyl-L-.alpha.-glutamyl-L-.alpha.-aspartyl-L-prolyl-L-tyrosyl-S-[1-[6-[[2-(4-aminophenyl)ethyl]amino]-6-oxohexyl]-2,5-dioxo-3-pyrrolidinyl]- (9CI) (CA INDEX NAME)

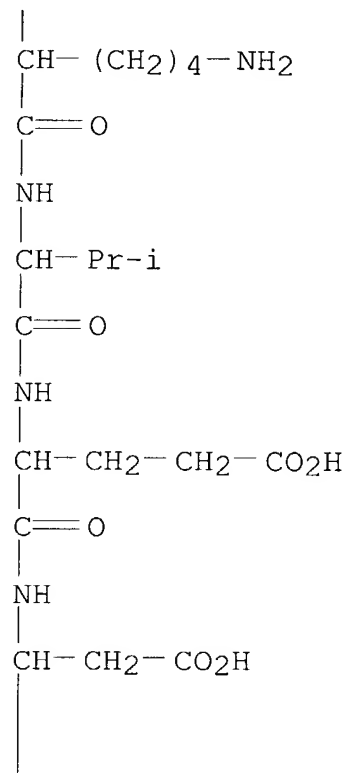
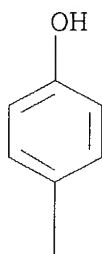
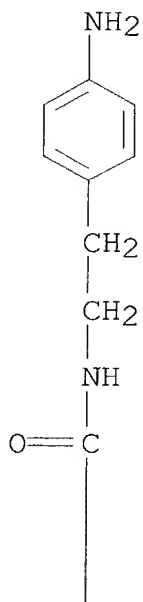
PAGE 1-A



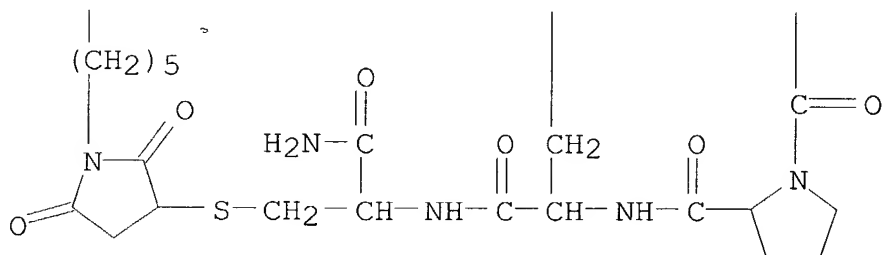
PAGE 2-A



PAGE 3-A



PAGE 4-A



CC 3-2 (Biochemical Genetics)
 Section cross-reference(s): 6

IT **Proteins**

(NLS (nuclear location signal sequence)-contg.; evaluation of nuclear localization of plasmid DNA-nuclear localization signal peptide conjugate)

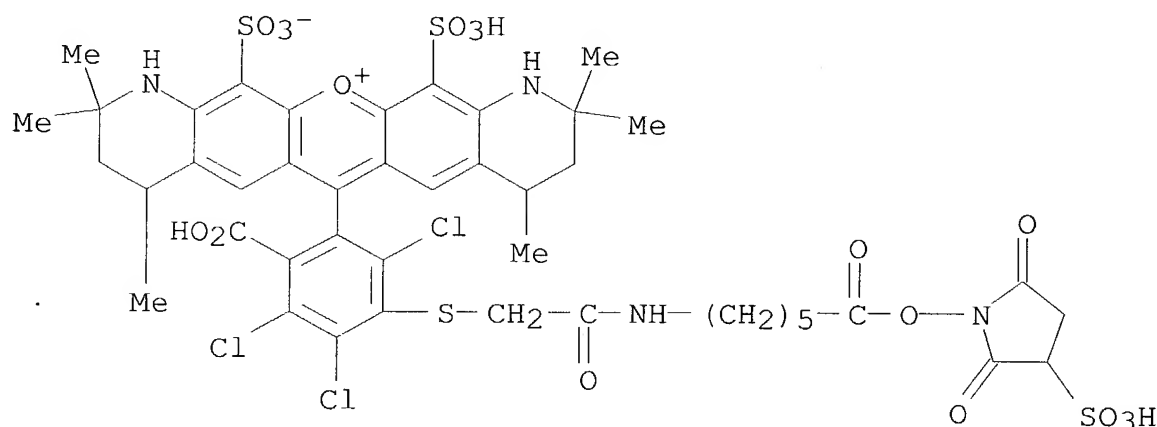
- IT **Polyoxyalkylenes**, biological studies
(PEG spacer; plasmid DNA-nuclear localization signal peptide conjugation via either short or long spacer)
- IT Molecular association
(assocn. of plasmid DNA-nuclear localization signal peptide conjugate with nuclear transport **proteins** importin .alpha. and .beta.)
- IT **Proteins**
(karyopherin .alpha.; assocn. of plasmid DNA-nuclear localization signal peptide conjugate with nuclear transport **proteins** importin .alpha. and .beta.)
- IT **Proteins**
(karyopherin .beta.; assocn. of plasmid DNA-nuclear localization signal peptide conjugate with nuclear transport **proteins** importin .alpha. and .beta.)
- IT 25322-68-3P, Poly(ethylene glycol)
(PEG spacer; plasmid DNA-nuclear localization signal peptide conjugation via either short or long spacer)
- IT **486397-36-8DP**, conjugated to plasmid pGL3 or pGFP
(evaluation of nuclear localization of plasmid DNA-nuclear localization signal peptide conjugate)

L98 ANSWER 5 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:21796 Methods and compositions related to tagging of membrane surface **proteins**. Alroy, Iris; Moskowicz, Haim; Reiss, Yuval; Shoham, Benjamin A. (Proteologics, Inc., USA). PCT Int. Appl. WO 2002099077 A2 20021212, 99 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-US18000 20020606. PRIORITY: US 2001-PV296334 20010606.

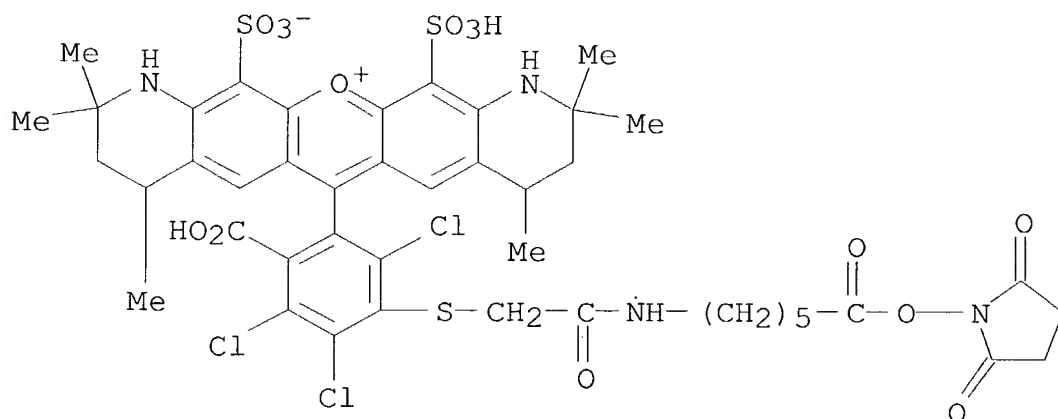
- AB The invention relates to methods and reagents for selectively labeling membrane surface **proteins** using a labeling agent. The label may be used to isolate preps. of membrane surface **proteins**. Preps. of membrane surface **proteins** may be **analyzed** by a variety of high-throughput techniques to allow rapid profiling of membrane surface **protein** compn.
- IT **477876-57-6 477876-66-7**
(methods and compns. related to tagging of membrane surface **proteins**)
- RN 477876-57-6 HCA

CN Pyrano[3,2-g:5,6-g']diquinolin-13-ium, 6-[2-carboxy-3,4,6-trichloro-5-[[2-[[6-[(2,5-dioxo-3-sulfo-1-pyrrolidinyl)oxy]-6-oxohexyl]amino]-2-oxoethyl]thio]phenyl]-1,2,3,4,8,9,10,11-octahydro-2,2,4,8,10,10-hexamethyl-12,14-disulfo-, inner salt (9CI) (CA INDEX NAME)



RN 477876-66-7 HCA

CN Pyrano[3,2-g:5,6-g']diquinolin-13-ium, 6-[2-carboxy-3,4,6-trichloro-5-[[2-[[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]amino]-2-oxoethyl]thio]phenyl]-1,2,3,4,8,9,10,11-octahydro-2,2,4,8,10,10-hexamethyl-12,14-disulfo-, inner salt (9CI) (CA INDEX NAME)



IC ICM C12N

CC 9-14 (Biochemical Methods)

Section cross-reference(s): 6

ST surface **protein** label tagging proteome sample prepn

IT Gel electrophoresis

(SDS; methods and compns. related to tagging of membrane surface **proteins**)

- IT **Proteins**
(SU (surface); methods and compns. related to tagging of membrane surface **proteins**)
- IT Chelating agents
(divalent; methods and compns. related to tagging of membrane surface **proteins**)
- IT Animal cell
- Disease, animal
- Disulfide** group
- Eukaryota
- Fluorescent substances
- Labels
- Linking agents
- Mass spectrometry**
- Organelle
- Protein** motifs
- Radioactive** substances
- Reduction
- Sample preparation
- Virus
- Washing
(methods and compns. related to tagging of membrane surface **proteins**)
- IT **Proteins**
(methods and compns. related to tagging of membrane surface **proteins**)
- IT Agglutinins and Lectins
(methods and compns. related to tagging of membrane surface **proteins**)
- IT Thiols (organic), properties
(methods and compns. related to tagging of membrane surface **proteins**)
- IT Extracellular matrix
(removal of; methods and compns. related to tagging of membrane surface **proteins**)
- IT Organelle
(vesicle; methods and compns. related to tagging of membrane surface **proteins**)
- IT 477876-55-4 477876-57-6 477876-59-8 477876-62-3
477876-64-5 477876-66-7 477937-32-9 477937-33-0
477937-34-1 477937-35-2 477937-36-3
(methods and compns. related to tagging of membrane surface **proteins**)
- IT 60-00-4, EDTA, uses
(methods and compns. related to tagging of membrane surface **proteins**)

137:348617 Acid-labile **isotope**-coded extractants: A Class of reagents for quantitative **mass spectrometric analysis** of complex **protein** mixtures. Qiu, Yongchang; Sousa, Eric A.; Hewick, Rodney M.; Wang, Jack H. (Proteomics/Protein Chemistry Department, Cambridge, MA, 02140, USA). Analytical Chemistry, 74(19), 4969-4979 (English) 2002. CODEN: ANCHAM. ISSN: 0003-2700. Publisher: American Chemical Society.

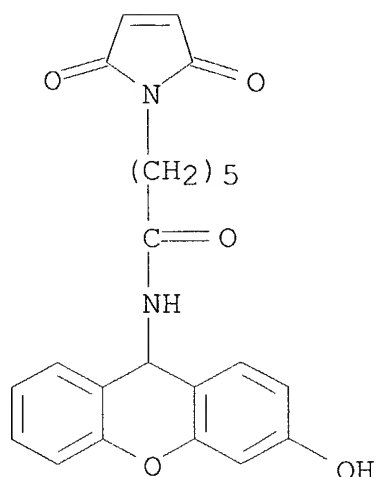
done
no
good

AB Quant. **mass spectrometry** using stable **isotope**-labeled tagging reagents such as **isotope**-coded affinity tags has emerged as a powerful tool for identification and relative **quantitation** of **proteins** in current proteomic studies. Here we describe an integrated approach using both automated two-dimensional liq. chromatog./**mass spectrometry** (2D-LC/MS) and a novel class of chem. modified resins, termed acid-labile **isotope**-coded extractants (ALICE), for quant. **mass spectrometric anal.** of **protein** mixts. ALICE contains a thiol-reactive group that is used to capture all **cysteine** (Cys)-contg. peptides from peptide mixts., an acid-labile linker, and a nonbiol. polymer. The acid-labile linker is synthesized in both heavy and light **isotope**-coded forms and therefore enables the direct relative **quantitation** of peptides/**proteins** through **mass spectrometric anal.** To test the ALICE method for quant. **protein anal.**, two model **protein** mixts. were fully reduced, alkylated, and **digested** in soln. sep. and then Cys-contg. peptides covalently captured by either light or heavy ALICE. The reacted light and heavy ALICE were mixed and washed extensively under rigorous conditions and the Cys-contg. peptides retrieved by mild acid-catalyzed elution. Finally, the eluted peptides were directly subjected to automated 2D-LC/MS for **protein identification** and LC/MS for accurate relative quantitation. Our initial study showed that **quantitation** of **protein** mixts. using ALICE was accurate. In addn., isolation of Cys-contg. peptides by the ALICE method was robust and specific and thus yielded very low background in **mass spectrometric** studies. Overall, the use of ALICE provides improved dynamic range and sensitivity for quant. **mass spectrometric anal.** of peptide or **protein** mixts.

IT 436144-21-7P
(acid-labile **isotope**-coded extractants for quant. **mass spectrometric anal.** of complex **protein** mixts.)

RN 436144-21-7 HCA

CN 1H-Pyrrole-1-hexanamide, 2,5-dihydro-N-(3-hydroxy-9H-xanthen-9-yl)-2,5-dioxo- (9CI) (CA INDEX NAME)



- CC 9-5 (Biochemical Methods)
- ST acid labile **isotope** coded extractant reagent **mass spectrometry**
- IT **Mass spectrometry**
 Process automation
 Sample preparation
 Simulation and Modeling, physicochemical
 (acid-labile **isotope**-coded extractants for quant. **mass spectrometric anal.** of complex **protein** mixts.)
- IT Peptides, analysis
Proteins
 (acid-labile **isotope**-coded extractants for quant. **mass spectrometric anal.** of complex **protein** mixts.)
- IT **Mass spectrometry**
 (liq. chromatog. combined with; acid-labile **isotope**-coded extractants for quant. **mass spectrometric anal.** of complex **protein** mixts.)
- IT Liquid chromatography
 (**mass spectrometry** combined with; acid-labile **isotope**-coded extractants for quant. **mass spectrometric anal.** of complex **protein** mixts.)
- IT Albumins, analysis
 (serum, bovine; acid-labile **isotope**-coded extractants for quant. **mass spectrometric anal.** of complex **protein** mixts.)
- IT **436144-21-7P**
 (acid-labile **isotope**-coded extractants for quant.)

mass spectrometric anal. of complex
protein mixts.)

L98 ANSWER 7 OF 28 HCA COPYRIGHT 2004 ACS on STN

137:306948 Multiplex detection of nucleic acid or **protein** by
mass spectrometry using a probe with a cleavable
photosensitive or chemi-activatable tag. Matray, Tracy J.;
Hernandez, Vincent S.; Chenna, Ahmed; Hooper, Herbert; Singh, Sharat
(Aclara Biosciences, Inc., USA). U.S. Pat. Appl. Publ. US
2002150927 A1 20021017, 25 pp., Cont.-in-part of U.S. Ser. No.
698,846. (English). CODEN: USXXCO. APPLICATION: US 2001-8593
20011109. PRIORITY: US 1999-303029 19990430; US 2000-561579
20000428; US 2000-602586 20000621; US 2000-684386 20001004; US
2000-698846 20001027.

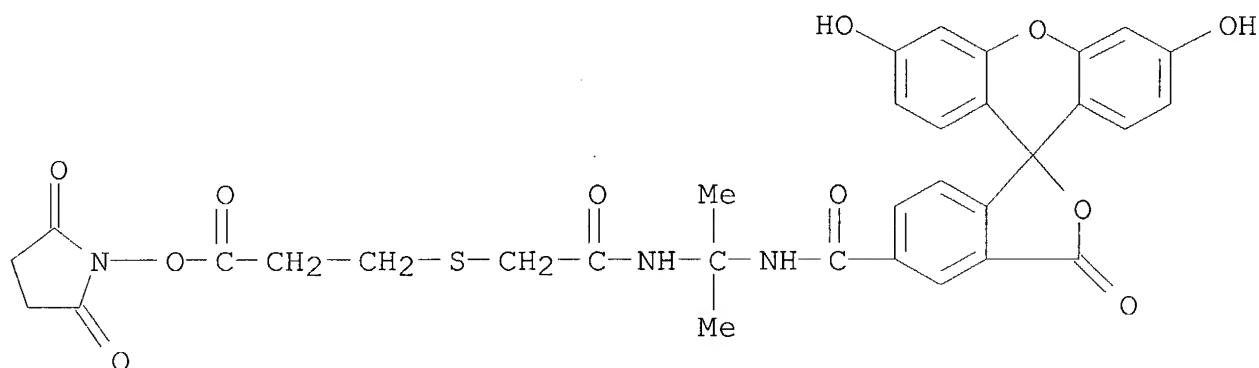
AB The invention provides a method for detecting a target analyte, by:
(a) contacting one or more target analytes with a set of first and
second binding reagents under conditions sufficient for binding of a
target analyte with the first and second binding reagents, each of
the first binding reagents contg. a cleavage-inducing moiety and a
target binding moiety, each of the second binding reagents contg. a
tagged probe having a mass modifier region attached to a target
binding moiety by a cleavable linkage, the cleavable linkage being
susceptible to cleavage when in proximity to an activated
cleavage-inducing moiety; (b) activating the cleavage-inducing
moiety to release a tag reporter, and (c) detecting a mass of the
tag reporter, the mass uniquely corresponding to a known target
analyte. The sequence contg. the SNP is exemplary of DNA sequences
of interest generally. Detection of multiple tag reporters using
mass spectrometry are described, including
synthesis of tag reagents and conjugation of sensitizer mols. to
assay reagents. A sandwich-type immunoassay for six cytokines is
carried out for the qualification and quantification of known
cytokine antigens. In this assay, a matched pair of antibodies
forms a sandwich around a cytokine antigen bringing the two
antibodies in close proximity to allow the singlet oxygen cleave the
cleavable linkage of the tagged probe.

IT 471244-00-5P 471244-01-6P 471244-02-7P
471244-03-8P 471244-04-9P 471244-05-0P
471244-06-1P 471244-07-2P 471244-08-3P
471244-09-4P

(as cleavable reporter conjugated to probe; methods for detecting
a plurality of analytes by **mass spectrometry**)

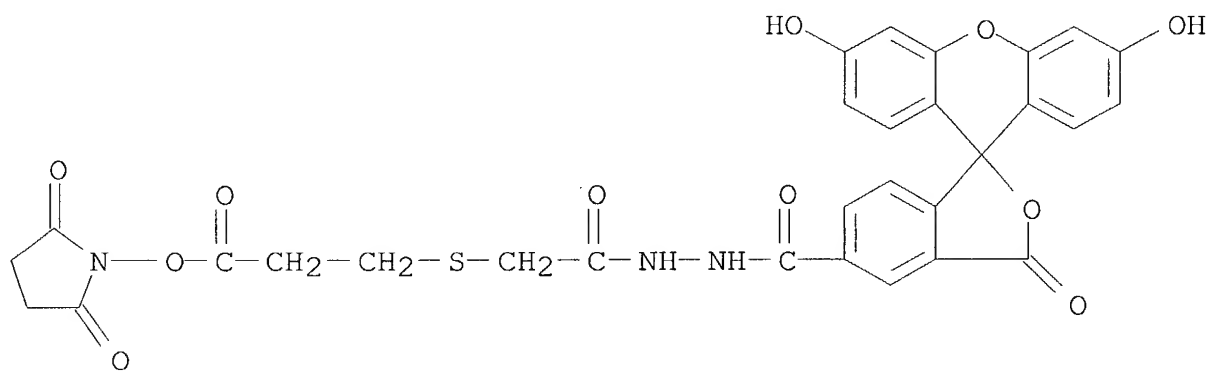
RN 471244-00-5 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-5-carboxamide,
N-[1-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-
oxopropyl]thio]acetyl]amino]-1-methylethyl]-3',6'-dihydroxy-3-oxo-
(9CI) (CA INDEX NAME)



RN 471244-01-6 HCA

CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxylic acid,
3',6'-dihydroxy-3-oxo-, 2-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-
oxopropyl]thio]acetyl]hydrazide (9CI) (CA INDEX NAME)

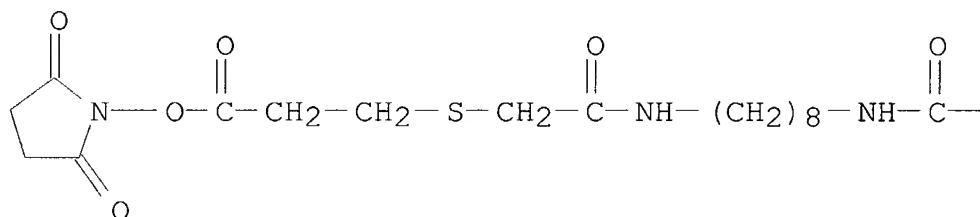


RN 471244-02-7 HCA

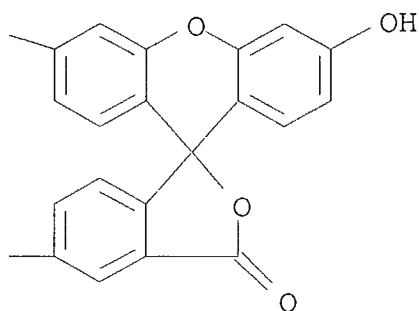
CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
N-[8-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-
oxopropyl]thio]acetyl]amino]octyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA
INDEX NAME)

PAGE 1-A

HO—

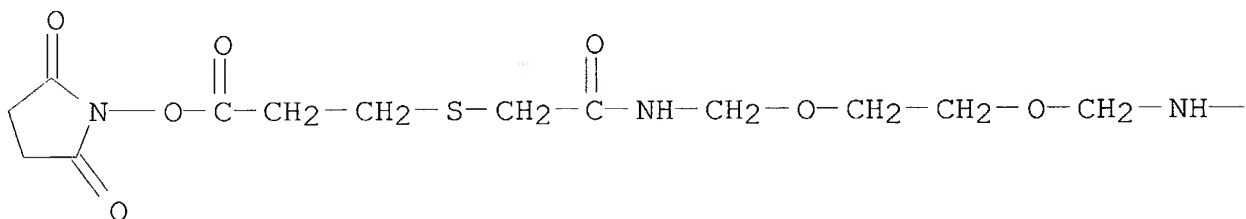


PAGE 1-B

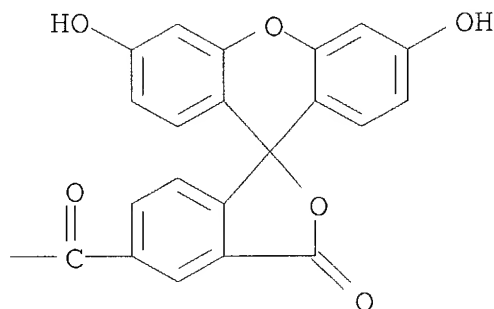


RN 471244-03-8 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
 N-[13-[(2,5-dioxo-1-pyrrolidinyl)oxy]-8,13-dioxo-2,5-dioxa-10-thia-7-
 azatridec-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A

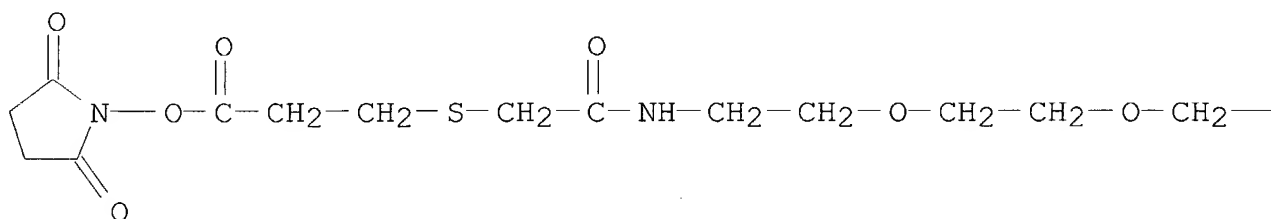


PAGE 1-B

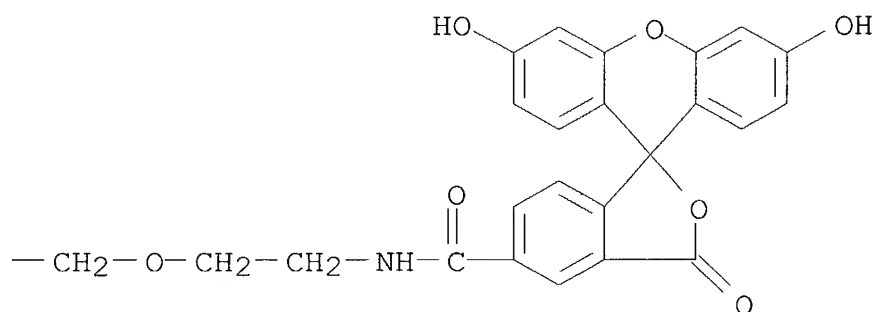


RN 471244-04-9 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
 N-[18-[(2,5-dioxo-1-pyrrolidinyl)oxy]-13,18-dioxo-3,6,9-trioxa-15-
 thia-12-azaooctadec-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX
 NAME)

PAGE 1-A



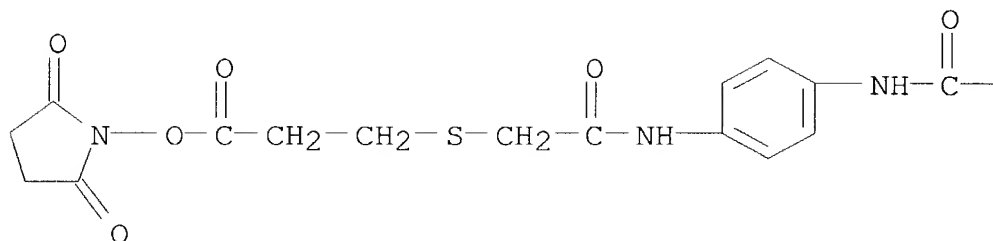
PAGE 1-B



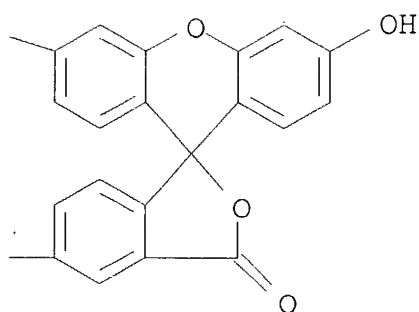
RN 471244-05-0 HCA
 CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-5-carboxamide,
 N-[4-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]phenyl]-3',6'-dihydroxy-3-oxo- (9CI)
 (CA INDEX NAME)

PAGE 1-A

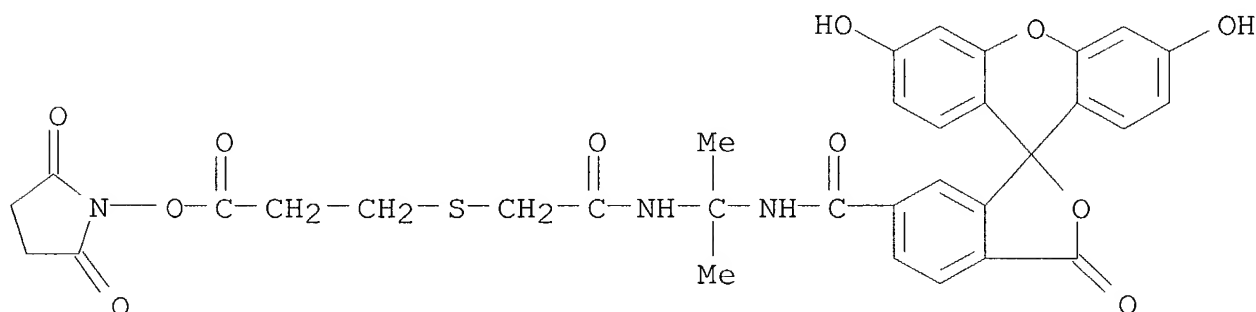
HO—



PAGE 1-B

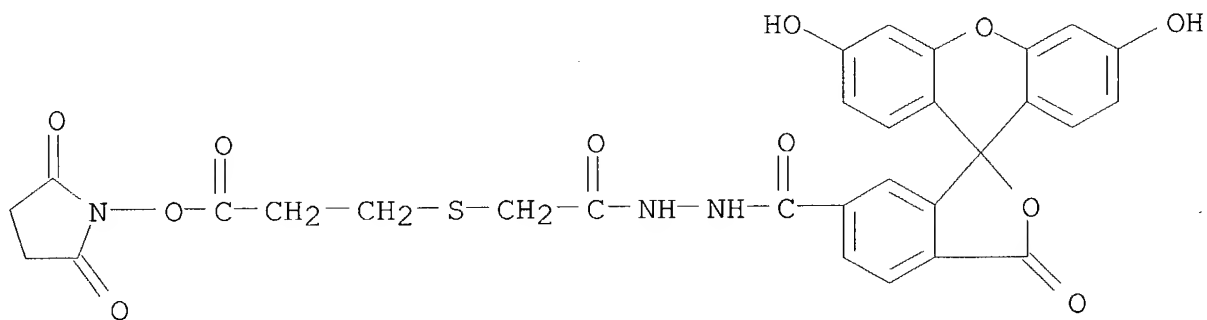


RN 471244-06-1 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-6-carboxamide,
 N-[1-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]-1-methylethyl]-3',6'-dihydroxy-3-oxo-
 (9CI) (CA INDEX NAME)



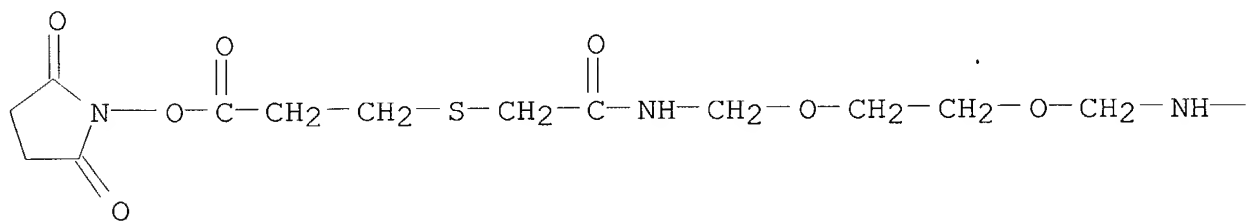
RN 471244-07-2 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-6-carboxylic acid,
3',6'-dihydroxy-3-oxo-, 2-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]hydrazide (9CI) (CA INDEX NAME)



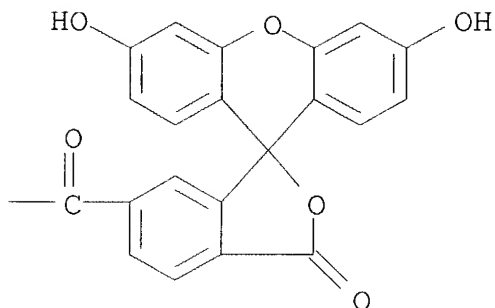
RN 471244-08-3 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-6-carboxamide,
N-[13-[(2,5-dioxo-1-pyrrolidinyl)oxy]-8,13-dioxo-2,5-dioxa-10-thia-7-azatridec-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)



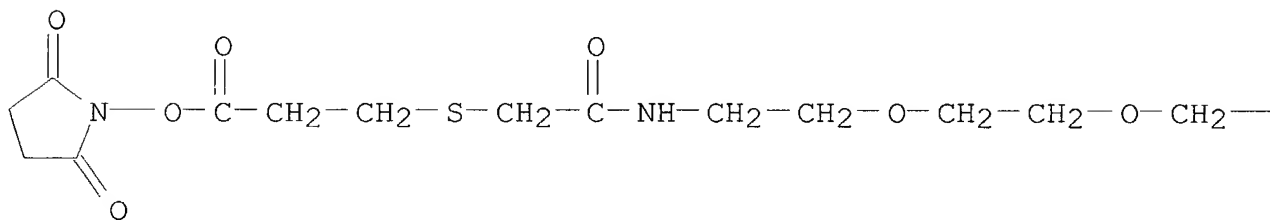
PAGE 1-A

PAGE 1-B

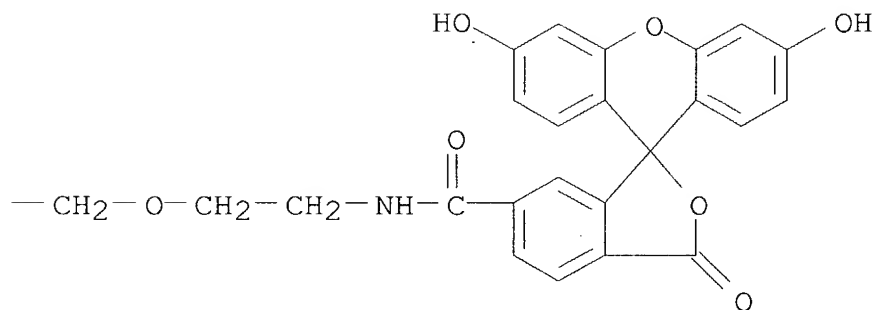


RN 471244-09-4 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-6-carboxamide,
 N-[18-[(2,5-dioxo-1-pyrrolidinyl)oxy]-13,18-dioxo-3,6,9-trioxa-15-
 thia-12-azaooctadec-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX
 NAME)

PAGE 1-A



PAGE 1-B



IC ICM C12Q001-68
NCL 435006000
CC 9-1 (Biochemical Methods)
Section cross-reference(s): 3, 6
ST SNP detection primer mass modifier cleavage **mass spectrometry**; multiplex **protein** analysis probe
cleavage photosensitizer **mass spectrometry**
IT **Proteins**
(A, conjugates with probe, as reporter; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Dyes**
(amine, tagged to the probe; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Antibodies**
(anti-ligand, conjugated with probe as reporter; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Cytokines**
Interleukin 10
Interleukin 4
Interleukin 6
Interleukin 8
Tumor necrosis factors
(antigen anal.; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Antibodies**
Antigens
Avidins
Ligands
Receptors
(as reporter, tagged to the probe; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Photoimaging materials**
(as reporter; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Nucleic acids**
(boronate-linked, mass-modified; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Chemistry**
(chem. compds., chemi-activated sensitizer, as reporter; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Metalloporphyrins**
(cleavable sensitizer tagged to the probe; methods for detecting a plurality of analytes by **mass spectrometry**)
IT **Polynucleotides**
(conjugates with probe, as reporter; methods for detecting a plurality of analytes by **mass spectrometry**)

- IT Bond
(covalent, nuclease-resistant, formed between probe and reporter;
methods for detecting a plurality of analytes by **mass spectrometry**)
- IT Aldehydes, analysis
(deriv., as cleavable reporter conjugated to probe; methods for
detecting a plurality of analytes by **mass spectrometry**)
- IT Light
(for reporter cleavage from the probe; methods for detecting a
plurality of analytes by **mass spectrometry**)
- IT Amides, analysis
(linkage between reporter and the probe; methods for detecting a
plurality of analytes by **mass spectrometry**)
- IT DNA microarray technology
Ion trap **mass spectrometry**
Mass spectrometry
Nucleic acid hybridization
Quadrupole **mass spectrometry**
Tandem **mass spectrometry**
Time-of-flight **mass spectrometry**
(methods for detecting a plurality of analytes by **mass spectrometry**)
- IT Carbohydrates, analysis
Lipids, analysis
Nucleic acids
Peptides, analysis
Polysaccharides, analysis
Proteins
(methods for detecting a plurality of analytes by **mass spectrometry**)
- IT Functional groups
(phosphodiester, linkage between reporter and the probe; methods
for detecting a plurality of analytes by **mass spectrometry**)
- IT Nucleic acids
(phosphoramidate-linked, mass-modified; methods for detecting a
plurality of analytes by **mass spectrometry**)
- IT Sulfonic acids, preparation
(released from reporter cleavage from the probe; methods for
detecting a plurality of analytes by **mass spectrometry**)
- IT Genetic polymorphism
(single nucleotide, detection of; methods for detecting a
plurality of analytes by **mass spectrometry**)
- IT Molecules
(small, anal. of; methods for detecting a plurality of analytes
by **mass spectrometry**)

IT Probes (nucleic acid)
 (tagged with mass modifier; methods for detecting a plurality of analytes by **mass spectrometry**)

IT Nucleic acids
 (thiophosphate-linked, mass-modified; methods for detecting a plurality of analytes by **mass spectrometry**)

IT Interferons
 (.gamma., antigen anal.; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 6066-82-6, N-Hydroxysuccinimide
 (as cleavable reporter conjugated to probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 151890-73-2P 412319-46-1P 471244-10-7P 471244-11-8P
 471244-12-9P 471244-13-0P 471244-14-1P 471244-15-2P
 471244-16-3P 471244-17-4P 471244-18-5P 471244-19-6P 471244-20-9P
 471244-21-0P 471244-22-1P 471244-23-2P 471244-24-3P
 471244-25-4P 471244-26-5P 471244-27-6P
 (as cleavable reporter conjugated to probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 471244-00-5P 471244-01-6P 471244-02-7P
 471244-03-8P 471244-04-9P 471244-05-0P
 471244-06-1P 471244-07-2P 471244-08-3P
 471244-09-4P
 (as cleavable reporter conjugated to probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 9013-20-1, Streptavidin
 (as reporter, tagged to the probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 58-85-5D, Biotin, conjugates with oligopeptides
 (as reporter; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 61-73-4, Methylene blue
 (cleavable sensitizer tagged to the probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 37228-74-3, Exonuclease
 (for reporter cleavage from the probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 9026-81-7, Nuclease
 (for tag cleavage from the probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 6303-21-5, Phosphinic acid
 (linkage between reporter and the probe; methods for detecting a plurality of analytes by **mass spectrometry**)

IT 119-61-9D, Benzophenone, conjugates with nucleic acid probes
 492-22-8D, 9-Thioxanthone, conjugates with nucleic acid probes
 523-27-3D, 9,10-Dibromoanthracene, conjugates with nucleic acid probes
 9003-99-0D, Myeloperoxidase, conjugates with nucleic acid probes
 9055-20-3D, Chloroperoxidase, conjugates with nucleic acid probes

- probes 17372-87-1D, Eosin, conjugates with nucleic acid probes
(methods for detecting a plurality of analytes by **mass spectrometry**)
- IT 107-96-0, 3-Mercaptopropionic acid 3301-79-9, 6-Carboxyfluorescein
39028-27-8 76823-03-5, 5-Carboxyfluorescein
(methods for detecting a plurality of analytes by **mass spectrometry**)
- IT 7782-44-7, Oxygen, analysis
(singlet, release from the reporter cleavage from the probe;
methods for detecting a plurality of analytes by **mass spectrometry**)

L98 ANSWER 8 OF 28 HCA COPYRIGHT 2004 ACS on STN
137:43912 Acid-labile **isotope**-coded extractant (ALICE) and its
use in quantitative **mass spectrometric analysis** of **protein** mixtures. Qiu, Yongchang;
Wang, Jack H.; Hewick, Rodney M. (Genetics Institute, Inc., USA).
PCT Int. Appl. WO 2002048717 A2 20020620, 44 pp. DESIGNATED STATES:
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM,
HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA,
ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG,
CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML,
MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2.
APPLICATION: WO 2001-US50745 20011022. PRIORITY: US 2000-PV242643
20001023.

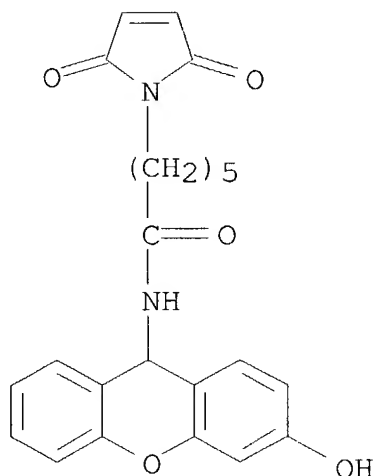
- AB The invention concerns a method which provides novel compds., termed
acid-labile **isotope**-coded extractants (ALICE), for quant.
mass spectrometric anal. of
protein mixts. The compds. contain a thiol-reactive group
that is used to capture **cysteine**-contg. **peptides**
from all **peptide** mixts., an acid-labile linker, and a
non-biol. polymer. One of the two acid-labile linkers is
isotopically labeled and therefore enables the direct
quantitation of **peptides/proteins**
through **mass spectrometric anal.** Because no
functional **proteins** are required to capture
peptides, a higher percentage of org. solvent can be used to
solubilize the **peptides**, particularly hydrophobic
peptides, through the binding, washing and eluting steps,
thus permitting much better recovery of **peptides**.
Moreover, since the **peptides** are covalently linked to the
non-biol. polymer (ALICE), more stringent washing is allowed in
order to completely remove non-specifically bound species. Finally,
peptides captured by ALICE are readily eluted from the
polymer support under mild acid condition with high yield and permit

the direct down stream **mass spectrometric** anal.
without any further sample manipulation. In combination with our
novel dual column two dimensional liq. chromatog.- **mass**
spectrometry (2D-LC-MS/MS) design, the
ALICE procedure proves to a general approach for quant. **mass**
spectrometric anal. of **protein** mixts.
with better dynamic range and sensitivity.

IT 436144-21-7D, reaction with polymers 436144-22-8D,
reaction with polymers
(acid-labile **isotope**-coded extractant (ALICE) and use
in quant. **mass spectrometric** anal.
of **protein** mixts.)

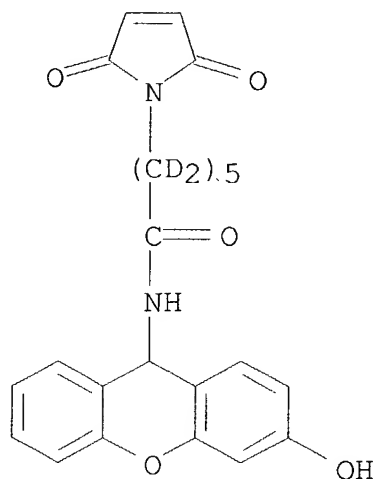
RN 436144-21-7 HCA

CN 1H-Pyrrole-1-hexanamide, 2,5-dihydro-N-(3-hydroxy-9H-xanthen-9-yl)-
2,5-dioxo- (9CI) (CA INDEX NAME)



RN 436144-22-8 HCA

CN 1H-Pyrrole-1-hexanamide-.alpha.,.alpha.,.beta.,.beta.,.gamma.,.gamma
.,.delta.,.delta.,.epsilon.,.epsilon.-d10, 2,5-dihydro-N-(3-hydroxy-
9H-xanthen-9-yl)-2,5-dioxo- (9CI) (CA INDEX NAME)



IT 7782-39-0, Deuterium, properties 9003-53-6
 , Polystyrene
 (acid-labile isotope-coded extractant (ALICE) and use
 in quant. mass spectrometric anal.
 of protein mixts.)
 RN 7782-39-0 HCA
 CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

RN 9003-53-6 HCA
 CN Benzene, ethenyl-, homopolymer (9CI) (CA INDEX NAME)
 CM 1
 CRN 100-42-5
 CMF C8 H8

$\text{H}_2\text{C}=\text{CH}-\text{Ph}$

IC ICM G01N033-68
 ICS G01N033-58; G01N033-532; C07D405-12
 CC 9-16 (Biochemical Methods)
 Section cross-reference(s): 6
 ST ALICE acid labile isotope coded extractant mass
 spectrometry protein; high throughput
 protein cysteine peptide HPLC
 mass spectrometry
 IT Polymers, analysis

(ALICE (acid-labile **isotope**-coded extractant);
acid-labile **isotope**-coded extractant (ALICE) and use in
quant. **mass spectrometric anal.** of
protein mixts.)

- IT **Mass spectrometry**
(HPLC combined with; acid-labile **isotope**-coded
extractant (ALICE) and use in quant. **mass**
spectrometric anal. of protein
mixts.)
- IT **Digestion, chemical**
 - Disulfide group**
 - High throughput screening
 - Mass spectrometry**
 - Process automation
 - Protein degradation**
 - Reduction
 - Sulfhydryl group
 - Tandem mass spectrometry**
 - Test kits
 - Washing
 - (acid-labile **isotope**-coded extractant (ALICE) and use
in quant. **mass spectrometric anal.**
of protein mixts.)
- IT **Proteins**
 - (acid-labile **isotope**-coded extractant (ALICE) and use
in quant. **mass spectrometric anal.**
of protein mixts.)
- IT **Reagents**
 - (acid-labile **isotope**-coded extractant (ALICE) and use
in quant. **mass spectrometric anal.**
of protein mixts.)
- IT **Enzymes, uses**
 - (acid-labile **isotope**-coded extractant (ALICE) and use
in quant. **mass spectrometric anal.**
of protein mixts.)
- IT **Isotopes**
 - Polyoxyalkylenes, properties**
 - (acid-labile **isotope**-coded extractant (ALICE) and use
in quant. **mass spectrometric anal.**
of protein mixts.)
- IT **Peptides, analysis**
 - (cysteine-contg.; acid-labile **isotope**-coded
extractant (ALICE) and use in quant. **mass**
spectrometric anal. of protein
mixts.)
- IT **Mass spectrometry**
 - (liq. chromatog. combined with; acid-labile **isotope**
-coded extractant (ALICE) and use in quant. **mass**

spectrometric anal. of protein
mixts.)

IT HPLC

Liquid chromatography

(mass spectrometry combined with; acid-labile
isotope-coded extractant (ALICE) and use in quant.
mass spectrometric anal. of
protein mixts.)

IT Albumins, analysis

(serum; acid-labile isotope-coded extractant (ALICE)
and use in quant. mass spectrometric
anal. of protein mixts.)

IT Halogen compounds

(.alpha.-halo-acetyl; acid-labile isotope-coded
extractant (ALICE) and use in quant. mass
spectrometric anal. of protein
mixts.)

IT 436144-21-7D, reaction with polymers 436144-22-8D,
reaction with polymers

(acid-labile isotope-coded extractant (ALICE) and use
in quant. mass spectrometric anal.
of protein mixts.)

IT 2949-92-0 9002-07-7, Trypsin

(acid-labile isotope-coded extractant (ALICE) and use
in quant. mass spectrometric anal.
of protein mixts.)

IT 541-59-3, Maleimide 7782-39-0, Deuterium,
properties 9003-53-6, Polystyrene 25322-68-3,
Polyethylene glycol

(acid-labile isotope-coded extractant (ALICE) and use
in quant. mass spectrometric anal.
of protein mixts.)

IT 438064-53-0

(unclaimed protein sequence; acid-labile
isotope-coded extractant (ALICE) and its use in quant.
mass spectrometric anal. of
protein mixts.)

IT 81183-26-8 435314-09-3 435314-15-1 435314-17-3 437984-21-9
437984-22-0 437984-23-1 437984-24-2 437984-25-3 437984-26-4
437984-27-5 437984-28-6 437984-29-7 437984-30-0 437984-31-1

(unclaimed sequence; acid-labile isotope-coded
extractant (ALICE) and its use in quant. mass
spectrometric anal. of protein
mixts.)

L98 ANSWER 9 OF 28 HCA COPYRIGHT 2004 ACS on STN

137:17454 Isotope-coded ionization-enhancing reagents (ICIER)
for high-throughput protein identification and

Wallenhorst 10/045,170

quantitation using matrix-assisted laser desorption ionization mass spectrometry. Qiu, Yongchang;

Wang, Jack H.; Hewick, Rodney M. (Genetics Institute, LLC, USA).
PCT Int. Appl. WO 2002046770 A2 20020613, 45 pp. DESIGNATED STATES:

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2.

APPLICATION: WO 2001-US50744 20011022. PRIORITY: US 2000-PV242645 20001023.

The invention concerns arginine-contg. **cysteine**-modifying compds. useful for MALDI-MS anal. of

proteins are provided. These compds. termed **isotope**-coded ionization enhancement reagents (ICIER) can provide ionization enhancement in MALDI-MS, relative quantitation, and addnl. database searching constraints at the same time without any extra sample manipulation. More specifically, ICIER increase the ionization efficiency of **cysteine**-contg. **peptides** by attachment of a guanidino functional group. ICIER also increase the overall hydrophilicity of these **peptides** due the hydrophilic nature of ICIER and thus increase the percentage of recovery of these **peptides** during sample handling and processing such as in-gel digestion or liq. chromatog. Finally, a combination of both light and heavy ICIER provides an accurate way to obtain relative quantitation of **proteins** by MALDI-MIS and addnl. database searching constraints (no. of **cysteine** residues in every single **peptide** peak) to increase the confidence of protein identification by peptide mass mapping.

IT 7782-39-0, Deuterium, uses
(isotope-coded ionization-enhancing reagents (ICIER)
for high-throughput protein identification
and quantitation using matrix-assisted laser desorption
ionization mass spectrometry)

RN 7782-39-0 HCA
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IT 52-90-4, Cysteine, properties
(isotope-coded ionization-enhancing reagents (ICIER)
for high-throughput protein identification

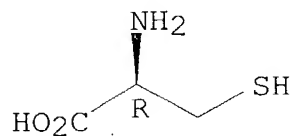
date no good

and **quantitation** using matrix-assisted laser desorption
ionization **mass spectrometry**)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IC ICM G01N033-68

CC 9-16 (Biochemical Methods)

Section cross-reference(s): 6

ST ionization reagent high throughput screening **protein MALDI
mass spectrometry**

IT Gel electrophoresis

(PAGE; **isotope**-coded ionization-enhancing reagents
(ICIER) for high-throughput **protein
identification and quantitation** using
matrix-assisted laser desorption ionization **mass
spectrometry**)

IT **Peptides**, analysis

(**cysteine**-contg.; **isotope**-coded
ionization-enhancing reagents (ICIER) for high-throughput
protein identification and quantitation
using matrix-assisted laser desorption ionization **mass
spectrometry**)

IT Functional groups

(guanidino group; **isotope**-coded ionization-enhancing
reagents (ICIER) for high-throughput **protein
identification and quantitation** using
matrix-assisted laser desorption ionization **mass
spectrometry**)

IT Amide group

Amino group

Carboxyl group

Chemical chains

Digestion, chemical

Disulfide group

High throughput screening

Ionization

Labels

Mass spectrometry

Molecular association

Radiochemical analysis

Sample preparation

Sulfhydryl group

Test kits

(**isotope**-coded ionization-enhancing reagents (ICIER)
for high-throughput **protein identification**
and **quantitation** using matrix-assisted laser desorption
ionization **mass spectrometry**)

IT **Peptides, analysis**

Proteins

(**isotope**-coded ionization-enhancing reagents (ICIER)
for high-throughput **protein identification**
and **quantitation** using matrix-assisted laser desorption
ionization **mass spectrometry**)

IT **Isotopes**

(**isotope**-coded ionization-enhancing reagents (ICIER)
for high-throughput **protein identification**
and **quantitation** using matrix-assisted laser desorption
ionization **mass spectrometry**)

IT **Reagents**

(**isotope**-coded ionization-enhancing reagents (ICIER)
for high-throughput **protein identification**
and **quantitation** using matrix-assisted laser desorption
ionization **mass spectrometry**)

IT **Functional groups**

(maleimide; **isotope**-coded ionization-enhancing reagents
(ICIER) for high-throughput **protein**
identification and **quantitation** using
matrix-assisted laser desorption ionization **mass**
spectrometry)

IT **Laser ionization mass spectrometry**

(photodesorption, matrix-assisted; **isotope**-coded
ionization-enhancing reagents (ICIER) for high-throughput
protein identification and **quantitation**
using matrix-assisted laser desorption ionization **mass**
spectrometry)

IT **Laser desorption mass spectrometry**

(photoionization, matrix-assisted; **isotope**-coded
ionization-enhancing reagents (ICIER) for high-throughput
protein identification and **quantitation**
using matrix-assisted laser desorption ionization **mass**
spectrometry)

IT **Functional groups**

(.alpha.-haloacetyl; **isotope**-coded ionization-enhancing
reagents (ICIER) for high-throughput **protein**
identification and **quantitation** using
matrix-assisted laser desorption ionization **mass**
spectrometry)

IT 7782-39-0, Deuterium, uses

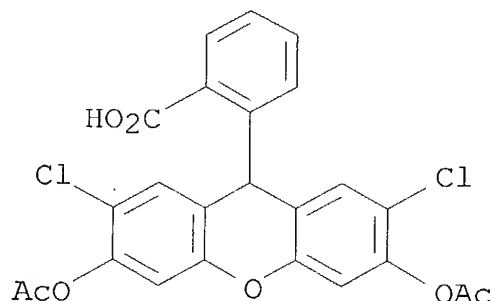
- (isotope-coded ionization-enhancing reagents (ICIER) for high-throughput **protein identification** and **quantitation** using matrix-assisted laser desorption ionization **mass spectrometry**)
- IT 434335-16-7P 434335-17-8P 434335-18-9P 434335-19-0P
434335-20-3P
- (isotope-coded ionization-enhancing reagents (ICIER) for high-throughput **protein identification** and **quantitation** using matrix-assisted laser desorption ionization **mass spectrometry**)
- IT 9001-92-7, Proteinase
- (isotope-coded ionization-enhancing reagents (ICIER) for high-throughput **protein identification** and **quantitation** using matrix-assisted laser desorption ionization **mass spectrometry**)
- IT 52-90-4, Cysteine, properties
- (isotope-coded ionization-enhancing reagents (ICIER) for high-throughput **protein identification** and **quantitation** using matrix-assisted laser desorption ionization **mass spectrometry**)
- IT 161181-39-1 435313-81-8 435313-83-0 435313-85-2 435313-87-4
435313-89-6 435313-91-0 435313-93-2 435313-95-4 435313-97-6
435313-99-8 435314-01-5 435314-03-7 435314-05-9 435314-07-1
435314-09-3 435314-12-8 435314-14-0 435314-15-1 435314-16-2
435314-17-3 435314-18-4 435314-19-5 435314-25-3 435314-27-5
- (unclaimed sequence; isotope-coded ionization-enhancing reagents (ICIER) for high-throughput **protein identification** and **quantitation** using matrix-assisted laser desorption ionization **mass spectrometry**)

08 ANSWER 10 OF 28 HCA COPYRIGHT 2004 ACS on STN
36:366139 Labeled peptides, proteins and antibodies and processes and intermediates useful for their preparation. Hahn, Klaus M.; Touthkine, Alexei; Muthyala, Rajeev; Kraynov, Vadim; Bark, Steven J.; Burton, Dennis R.; Chamberlain, Chester (USA). U.S. Pat. Appl. Publ. US 2002055133 A1 20020509, 54 pp., Cont.-in-part of Appl. No. PCT/US2000/26821. (English). CODEN: USXXCO. APPLICATION: US 2001-839577 20010420. PRIORITY: US 2000-PV218113 20000713; WO 2000-US26821 20000929.

The invention provides peptide synthons having protected functional groups for attachment of desired moieties (e.g. functional mols. or probes). Also provided are peptide conjugates prep'd. from such synthons, and synthon and conjugate prepn. methods including procedures for identifying the optimum probe attachment site. Biosensors are provided having environmentally sensitive dyes that can locate specific biomols. within living cells and detect chem. and physiol. changes in those biomols. as the living cell is moving,

metabolizing and reacting to its environment. Methods are included for detecting GTP activation of a Rho GTPase protein using polypeptide biosensors. When the biosensor binds GTP-activated Rho GTPase protein, the environmentally sensitive dye emits a signal of a different lifetime, intensity or wavelength than when not bound. New fluorophores whose fluorescence responds to environmental changes are also provided that have improved detection and attachment properties, and that can be used in living cells, or in vitro.

- IT 4091-99-ODP, DCFH, conjugates
(DCFH; labeled peptides and proteins and antibodies and processes and intermediates useful in their prepn.)
- RN 4091-99-0 HCA
- CN Benzoic acid, 2-[3,6-bis(acetyloxy)-2,7-dichloro-9H-xanthen-9-yl]-
(9CI) (CA INDEX NAME)



- IC G01N033-53; G01N033-537; G01N033-543; C07D417-02; C07K014-435
- NCL 435079200
- CC 9-14 (Biochemical Methods)
Section cross-reference(s): 1, 7, 34, 41
- IT Imaging
(FLAIR (fluorescent activation **indicator** for Rho **proteins**); labeled peptides and proteins and antibodies and processes and intermediates useful in their prepn.)
- IT 4091-99-ODP, DCFH, conjugates
(DCFH; labeled peptides and proteins and antibodies and processes and intermediates useful in their prepn.)
- IT 423205-43-0P
(amino acid sequence, cloning and site-specific **cysteine** mutagenesis of; labeled peptides and proteins and antibodies and processes and intermediates useful in their prepn.)

L98 ANSWER 11 OF 28 HCA COPYRIGHT 2004 ACS on STN

136:196571 Highly homogeneous molecular markers for electrophoresis.
Tadayoni-Rebek, Mitra; Amshey, Joseph W.; Rooney, Regina (Invitrogen Corporation, USA). PCT Int. Appl. WO 2002013848 A1 20020221, 64 pp.
DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR,

BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English).

CODEN: PIXXD2. APPLICATION: WO 2001-US25276 20010813. PRIORITY: US 2000-PV224345 20000811.

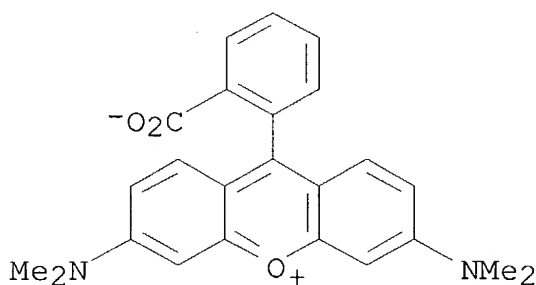
AB The invention relates to marker mols. for identifying phys. properties of mol. species sepd. by the use of electrophoretic systems. The invention further relates to methods for prep. and using marker mols. Peptide Cys-Leu-Lys(TMR)-Asp-Ala-Leu-Asp-Ala-Leu-Asp-Ala-Leu-Lys(TMR)-Asp-Ala was prepd. by solid phase peptide synthesis and ligated with a recombinant 95-amino acid maltose-binding **protein** to make a marker **protein** with pI 4.75.

IT 401466-24-8

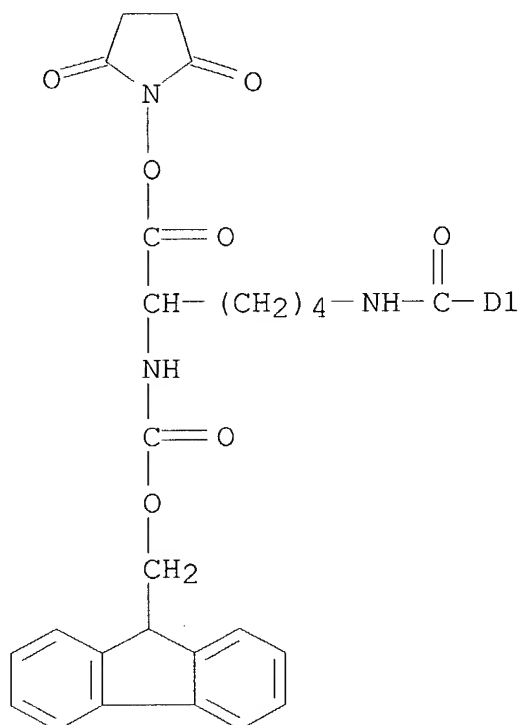
(highly homogeneous mol. markers for electrophoresis)

RN 401466-24-8 HCA

CN Xanthylium, 9-[2-carboxy-4(or 5)-[[[(5S)-6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-5-[[[(9H-fluoren-9-ylmethoxy)carbonyl]amino]-6-oxohexyl]amino]carbonyl]phenyl]-3,6-bis(dimethylamino)-, inner salt (9CI) (CA INDEX NAME)

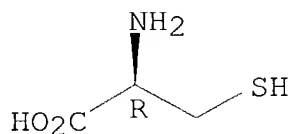


PAGE 2-A



IT 52-90-4, **Cysteine**, properties
 (labeling mol. contg. N-terminal; highly homogeneous mol. markers
 for electrophoresis)
 RN 52-90-4 HCA
 CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IC ICM A61K038-16
 CC 9-7 (Biochemical Methods)
 Section cross-reference(s): 34
 ST homogeneous mol marker electrophoresis; **protein** marker
 electrophoresis isoelec point; maltose binding **protein**
 ligation labeled peptide
 IT **Proteins**

- (MBP (maltose-binding **protein**), 95-amino acid, ligation with TMR-labeled peptide; highly homogeneous mol. markers for electrophoresis)
- IT Linking agents
(between label component and **protein** or nucleic acid; highly homogeneous mol. markers for electrophoresis)
- IT Gene
(for 95-amino acid maltose binding **protein**; highly homogeneous mol. markers for electrophoresis)
- IT **Proteins**
(highly homogeneous mol. markers for electrophoresis)
- IT Amino acids, preparation
Nucleic acids
Peptides, preparation
Proteins
(labeled; highly homogeneous mol. markers for electrophoresis)
- IT Peptides, preparation
(oligopeptides, labeled, prepn. and ligation to **protein**; highly homogeneous mol. markers for electrophoresis)
- IT **Test kits**
(**protein** marker kits; highly homogeneous mol. markers for electrophoresis)
- IT 401466-17-9 401466-24-8
(highly homogeneous mol. markers for electrophoresis)
- IT 52-90-4, **Cysteine**, properties
(labeling mol. contg. N-terminal; highly homogeneous mol. markers for electrophoresis)
- IT 401466-22-6P
(ligation with 95-amino acid maltose-binding **protein** to make marker **protein**; highly homogeneous mol. markers for electrophoresis)
- IT 401466-03-3P 401466-07-7P 401466-09-9P 401466-12-4P
401466-14-6P
(prepn. and ligation with maltose-binding **protein** to make marker **protein**; highly homogeneous mol. markers for electrophoresis)

L98 ANSWER 12 OF 28 HCA COPYRIGHT 2004 ACS on STN

136:163716 Labeled peptides, **proteins** and antibodies and processes and intermediates useful for their preparation. Hahn, Klaus M.; Touthkine, Alexei; Muthyala, Rajeev; Kraynov, Vadim; Bark, Steven J.; Burton, Dennis R.; Chamberlain, Chester (The Scripps Research Institute, USA). PCT Int. Appl. WO 2002008245 A2 20020131, 158 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,

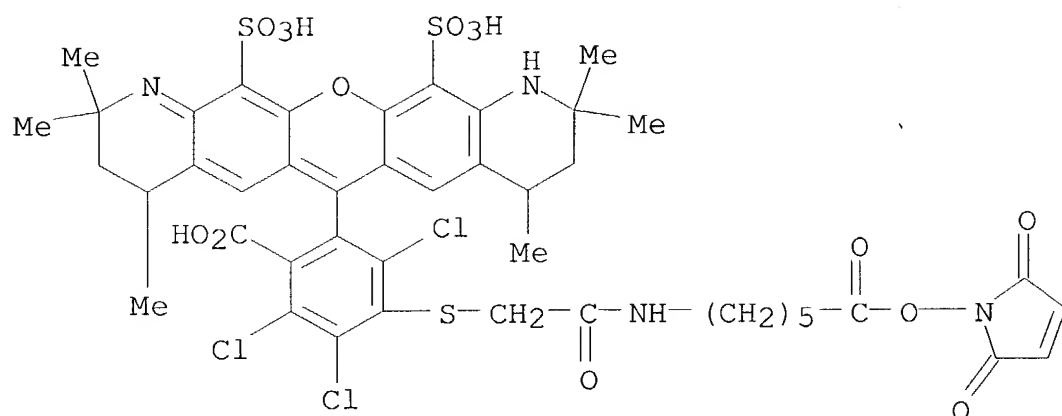
TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US22194 20010713. PRIORITY: US 2000-PV218113 20000713; WO 2000-US26821 20000929; US 2001-PV279302 20010328; US 2001-839577 20010420.

AB The invention provides peptide synthons having protected functional groups for attachment of desired moieties (e.g. functional mols. or probes). Also provided are peptide conjugates prep'd. from such synthons, and synthon and conjugate prep'n. methods including procedures for identifying optimum probe attachment sites. Biosensors are provided having functional mols. that can locate and bind to specific biomols. within living cells. Biosensors can detect chem. and physiol. changes in those biomols. as living cells are moving, metabolizing and reacting to its environment. Methods are included for detecting GTP activation of a Rho GTPase **protein** using polypeptide biosensors. When the biosensor binds GTP-activated Rho GTPase **protein**, an environmentally sensitive dye emits a signal of a different lifetime, intensity or wavelength than when not bound. New fluorophores whose fluorescence responds to environmental changes are also provided that have improved detection and attachment properties, and that can be used in living cells, or in vitro.

IT 393512-12-4
(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prep'n.)

RN 393512-12-4 HCA

CN Benzoic acid, 2,3,5-trichloro-4-[[2-[[6-[(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)oxy]-6-oxohexyl]amino]-2-oxoethyl]thio]-6-[1,3,4,8,9,10-hexahydro-2,2,4,8,10,10-hexamethyl-12,14-disulfo-2H-pyrano[3,2-g:5,6-g']diquinolin-6-yl]-, monosodium salt (9CI) (CA INDEX NAME)



● Na

IC ICM C07K001-00
 CC 9-14 (Biochemical Methods)
 Section cross-reference(s): 7, 15, 34, 41
 ST labeled peptide **protein** antibody prepn; biosensor
 targeting biomol living cell probe; GTP activation Rho GTPase
 detection polypeptide biosensor; fluorophore fluorescence probe
 environmental change living cell
 IT Animal cell line
 (3T3; labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)
 IT Fluorescent dyes
 (Alexa, conjugates with polypeptides; labeled peptides,
proteins and antibodies and processes and intermediates
 useful for prepn.)
 IT Imaging
 (FLAIR (fluorescent activation **indicator** for Rho
proteins); labeled peptides, **proteins** and
 antibodies and processes and intermediates useful for prepn.)
 IT Transcription factors
 (GCN4, peptide tag derived from leucine zipper of; labeled
 peptides, **proteins** and antibodies and processes and
 intermediates useful for prepn.)
 IT Histocompatibility antigens
 (HLA-B27, fusion **proteins** with GFP; labeled peptides,
proteins and antibodies and processes and intermediates
 useful for prepn.)
 IT Immunoglobulin receptors
 (IgE type I; labeled peptides, **proteins** and antibodies

- and processes and intermediates useful for prepn.)
- IT Resins
(MBHA; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Histocompatibility antigens
(MHC (major histocompatibility complex); labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Phycoerythrins
(P; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Phycoerythrins
(R-phycoerythrins, conjugates with peptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Imaging
(Rac activation in cells; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Wound healing
(Rac role in; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT G **proteins** (guanine nucleotide-binding **proteins**)
(Rac, polypeptide biosensor as p21-activated kinase peptide binding to; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(WASP (Wiskott-Aldrich syndrome **protein**), polypeptide biosensor as peptide of, binding to cdc42; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Functional groups
(aminooxy, peptide contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Neutrophil
(assay of cdc42 activity in cell lysates of stimulated; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Physics
(biophysics, probes; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(cellular, localization in living cells; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Allophycocyanins
Phycoerythrins
(conjugates with peptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

- IT Drugs
(conjugates with polypeptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Antibodies
Peptides, biological studies
Polynucleotides
Proteins
(conjugates; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(cyan fluorescent **protein**, conjugates, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Fluorescent dyes
(cyanine, conjugates with peptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Gene
(encoding fusion **proteins**; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(enhanced green fluorescent **protein**, conjugates, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(enhanced yellow green fluorescent **protein**, conjugates, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Cyanine dyes
(fluorescent, conjugates with peptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Fluorescent substances
(fluorophores, for detecting changes in responses of living cells to environment; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Immunoglobulins
(fragments, conjugates; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Rho **protein** (G **protein**)
(fusion **proteins** with fluorescent **proteins**; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT G **proteins** (guanine nucleotide-binding **proteins**)
(gene CDC42; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Rho **protein** (G **protein**)

(gene RhoA; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT **Proteins**

(green fluorescent, conjugates, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT Nucleic acids

(indicators for, conjugates with polypeptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT Biosensors

Blood serum

Cell

Cell migration

Endoplasmic reticulum

Fibroblast

Fluorescence

Fluorescence excitation

Fluorescence resonance energy transfer

Fluorescent dyes

Genetic vectors

Human

Phosphorescence

Phosphorescent substances

Signal transduction, biological

Stress, animal

Stress, microbial

Stress, plant

(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT Actins

Calmodulins

Myosins

(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT Peptides, biological studies

(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT DNA

Proteins

RNA

(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT Antibodies

Antigens

(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)

IT Platelet-derived growth factors

- (labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Nucleic acids
(labeled; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Antibodies
(labeled; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Peptides, biological studies
(labeled; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(labeled; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Protein motifs**
(leucine zipper, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Fusion **proteins** (chimeric **proteins**)
(of Rho GTPase **protein** and fluorescent **proteins** ; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Affinity
(of peptide conjugate for target; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Actins
(polymn., Rac1 activation localization at site of; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Ligands
(polypeptide-dye conjugates sensitive to binding by; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT pH
(polypeptide-dye conjugates sensitive to; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT ESR (electron spin resonance)
(probes, conjugates with polypeptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Protein motifs**
(**protein**-binding domain of p21-activated kinase 1, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT Phosphorylation, biological
(**protein**; labeled peptides, **proteins** and

- antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(red fluorescent **protein**, conjugates, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Sensors**
(responsive, conjugates with polypeptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Dyes**
(sensitive to pH or ligand binding or other, conjugates with polypeptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Cage compounds**
(sensors, conjugates with polypeptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Dyes**
(solvatochromic, conjugates with polypeptides; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Proteins**
(yellow green fluorescent **protein**, conjugates, polypeptide biosensor contg.; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Actinins**
(.alpha.-; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT **Lactoglobulins**
(.beta.-, labeling with tetramethylrhodamine N-hydroxysuccinimide ester; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 144713-51-9, Erk4 **protein** kinase
(Erk4 **protein** kinase; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 9059-32-9DP, GTPase, conjugates with fluorescent **proteins**
(GTP-activated Rho; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 394257-19-3P
(amino acid sequence of peptide tag derived from GCN4 leucine zipper; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 271795-11-0P
(amino acid sequence, C-terminal p21 binding domain peptide; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 393511-94-9P

- (amino acid sequence, N-terminal p21 binding domain peptide; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 394257-16-0
(amino acid sequence, as tag in cellular **protein** localization; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 394257-20-6P
(amino acid sequence, cloning and site-specific **cysteine** mutagenesis of; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 394257-21-7
(amino acid sequence; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 393512-08-8 393512-09-9 393512-10-2 393512-11-3
(as merocyanine dye; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 76-05-1, Trifluoroacetic acid, uses 5961-85-3,
Tris(2-carboxyethyl)phosphine
(in eliminating multiply-labeled side products; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 50-01-1P, Guanidine hydrochloride
(in improving yield of labeled product; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 9002-07-7, Trypsin 9004-07-3, .alpha.-Chymotrypsin
(labeled peptide cleavage with; labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 137632-07-6, Erk1 kinase 144713-50-8, Erk3 **protein** kinase
(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 137632-08-7, Erk2 kinase
(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 394257-19-3DP, tetramethylrhodamine-labeled
(labeled peptides, **proteins** and antibodies and processes and intermediates useful for prepn.)
- IT 65-61-2DP, Acridine Orange, conjugates with peptides 1239-45-8DP, Ethidium Bromide, conjugates with peptides 1325-87-7DP, Cascade Blue, conjugates with peptides 1461-15-0DP, Calcein, conjugates with peptides 2321-07-5DP, Fluorescein, conjugates with peptides 2768-89-0DP, Rhodamine X, conjugates with peptides 3520-42-1DP, Lissamine Rhodamine B, conjugates with peptides 7059-24-7DP, Chromomycin A3, conjugates with peptides 7240-37-1DP, 7-AAD, conjugates with peptides 10199-91-4DP, NBD, conjugates with

peptides 18378-89-7DP, Mithramycin, conjugates with peptides
 23491-45-4DP, Hoechst 33258, conjugates with peptides
 23491-52-3DP, Hoechst 33342, conjugates with peptides
 25535-16-4DP, Propidium Iodide, conjugates with peptides
 30230-57-0DP, conjugates with peptides 41085-99-8DP, conjugates
 with peptides 43070-85-5DP, Hydroxycoumarin, conjugates with
 peptides 47165-04-8DP, DAPI, conjugates with peptides
 51908-46-4DP, Dansyl aziridine, conjugates with peptides
 70281-37-7DP, Tetramethylrhodamine, conjugates with peptides
 76421-73-3DP, Monochlorobimane, conjugates with peptides
 76433-29-9DP, LDS 751, conjugates with peptides 82354-19-6DP,
 Texas Red, conjugates with peptides 82446-52-4DP, Lucifer Yellow,
 conjugates with peptides 96314-96-4DP, Indo-1, conjugates with
 peptides 96314-98-6DP, Fura-2, conjugates with peptides
 107091-89-4DP, Thiazole Orange, conjugates with peptides
 107347-53-5DP, TRITC, conjugates with peptides 112117-57-4DP,
 conjugates with peptides 123632-39-3DP, Fluo-3, conjugates with
 peptides 126208-12-6DP, Carboxy-SNARF-1, conjugates with peptides
 143245-02-7DP, conjugates with peptides 143413-84-7DP, TOTO-1,
 conjugates with peptides 143413-85-8DP, YOYO-1, conjugates with
 peptides 146368-15-2DP, Cy5, conjugates with peptides
 146368-16-3DP, Cy3, conjugates with peptides 149838-22-2DP, FM
 1-43, conjugates with peptides 153967-04-5DP, SNARF, conjugates
 with peptides 157199-59-2DP, TO-PRO-1, conjugates with peptides
 157199-63-8DP, TO-PRO-3, conjugates with peptides 165599-63-3DP,
 BODIPY-FL, conjugates with peptides 166196-17-4DP, TOTO-3,
 conjugates with peptides 169799-14-8DP, Cy7, conjugates with
 peptides 194100-76-0DP, SYTOX Green, conjugates with peptides
 204934-16-7DP, BODIPY TR, conjugates with peptides 237752-36-2DP,
 Red 613, conjugates with peptides 247145-11-5DP, Alexa-532,
 conjugates with peptides 287384-28-5DP, BODIPY TMR, conjugates
 with peptides 324767-53-5DP, SYTOX Orange, conjugates with
 peptides 396076-95-2DP, TruRed, conjugates with peptides
 396077-00-2DP, SYTOX Blue, conjugates with peptides

(labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 393511-95-0P

(labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 56-65-5, ATP, biological studies 86-01-1, GTP 22537-22-0,
 Magnesium ion, biological studies 142805-58-1, MEK kinase

(labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 393511-96-1DP, ditetramethylrhodamine-labeled 393511-97-2P

(labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 64-19-7, Acetic acid, uses 7440-66-6, Zinc, uses

(labeled peptides, **proteins** and antibodies and

processes and intermediates useful for prepn.)

IT 271795-07-4P 271795-10-9P 393511-92-7P 393511-93-8P
 393511-96-1P 394257-17-1P 394656-50-9P 394656-72-5P
 (labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 393511-93-8DP, tetramethylrhodamine-labeled 394656-50-9DP,
 tetramethylrhodamine-labeled 394679-45-9P
 (labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 1080-74-6, 3-(Dicyanomethylene)indan-1-one 1127-35-1 4229-44-1,
 N-Methylhydroxylamine hydrochloride 5292-43-3 13139-15-6
 17576-35-1, 1,3,3-Trimethoxy propene 27144-18-9 73259-81-1
 246256-50-8 271795-14-3 393512-00-0 393512-07-7
 393512-12-4
 (labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 271795-03-0P 271795-04-1P 271795-05-2P 393511-98-3DP,
 resin-bound 393511-99-4DP, resin-bound 393512-01-1P
 393512-04-4P 394257-18-2P
 (labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 393512-02-2P 393512-03-3P 393512-05-5P 393512-06-6P
 (labeled peptides, **proteins** and antibodies and
 processes and intermediates useful for prepn.)

IT 9059-32-9, GTPase
 (of Rho **protein**; labeled peptides, **proteins**
 and antibodies and processes and intermediates useful for prepn.)

IT 70-18-8, Glutathione, miscellaneous
 (peptide not; labeled peptides, **proteins** and antibodies
 and processes and intermediates useful for prepn.)

IT 177893-51-5P, p21-Activated kinase
 (polypeptide biosensor as peptide of, binding to Rac; labeled
 peptides, **proteins** and antibodies and processes and
 intermediates useful for prepn.)

IT 142243-02-5, MAP kinase
 (polypeptide biosensor; labeled peptides, **proteins** and
 antibodies and processes and intermediates useful for prepn.)

IT 394292-00-3 394292-01-4 394292-02-5 394292-03-6 394292-04-7
 394292-05-8 394292-06-9 394292-07-0 394292-08-1
 (unclaimed nucleotide sequence; labeled peptides,
proteins and antibodies and processes and intermediates
 useful for their prepn.)

IT 394291-97-5 394291-98-6 394291-99-7
 (unclaimed **protein** sequence; labeled peptides,
proteins and antibodies and processes and intermediates
 useful for their prepn.)

IT 394211-44-0 394211-45-1
 (unclaimed sequence; labeled peptides, **proteins** and

antibodies and processes and intermediates useful for their
prepn.)

L98 ANSWER 13 OF 28 HCA COPYRIGHT 2004 ACS on STN

136:147493 Compounds and methods of non-invasive diagnostic imaging.
Bridon, Dominique P.; Blanchard, Dominique; Ezrin, Alan M.;
Pouletty, Phillipe (Can.). U.S. Pat. Appl. Publ. US 2002018751 A1
20020214, 12 pp., Cont.-in-part of U.S. Ser. No. 588,912, abandoned.
(English). CODEN: USXXCO. APPLICATION: US 1999-327764 19990607.
PRIORITY: US 1993-137821 19931015; US 1994-237346 19940503; US
1995-477900 19950607; US 1996-588912 19960112.

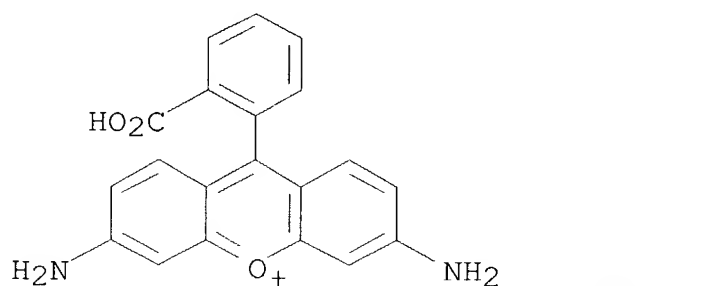
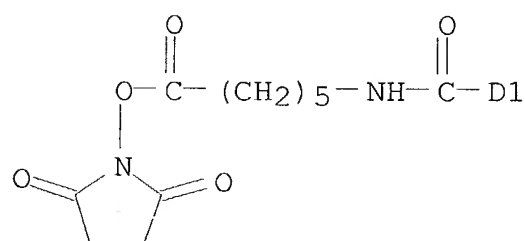
AB The invention concerns compns. and methods of non-invasive diagnosis
are provided. The imaging agents include a linking groups and a
reactive entity capable of reaction with a reactive functionality to
form a covalent bond therewith. The imaging agents may be in the
form of a bifunctional anchor mol. The bifunctional anchor mols.
have a functional group capable of activation which, when activated,
may form a covalent bond with a reactive functionality on a target
protein present in the mammalian vascular system, thereby
"anchoring" the mol. to that target **protein**. The
bifunctional anchors are also conjugated, either directly or
indirectly, to a diagnostic agent of interest which provides the
ability to diagnostically and non-invasively image the mammalian
vascular space. Vascular targets include both cellular- and
noncellular-assocd. **proteins** present in the mammalian
vascular system. The methods find use for numerous applications
arising from the ability to diagnostically image the mammalian
vascular space over an extended period of time or to preferentially
diagnostically image only a specific cell type or compartment of the
mammalian vascular space.

IT 244760-42-7

(compds. and methods of non-invasive diagnostic imaging)

RN 244760-42-7 HCA

CN Xanthylum, 3,6-diamino-9-[2-carboxy-4(or 5)-[[[6-[(2,5-dioxo-1-
pyrrolidinyl)oxy]-6-oxohexyl]amino]carbonyl]phenyl]-, chloride (9CI)
(CA INDEX NAME)

● Cl⁻

IC ICM A61K049-00
 NCL 424009100
 CC 9-14 (Biochemical Methods)
 Section cross-reference(s): 8, 14
 ST imaging diagnosis agent **radioisotope** mammal vascular
 covalent bond
 IT 35013-72-0 35898-04-5, biological studies 75501-17-6
 244760-42-7 292140-66-0
 (comps. and methods of non-invasive diagnostic imaging)

L98 ANSWER 14 OF 28 HCA COPYRIGHT 2004 ACS on STN
 135:223698 Proteomics based on selecting and quantifying **cysteine** containing **peptides** by covalent chromatography. Wang, S.; Regnier, F. E. (Department of Chemistry, Purdue University, Lafayette, IN, 47907, USA). Journal of Chromatography, A, 924(1-2), 345-357 (English) 2001. CODEN: JCRAEY. ISSN: 0021-9673. Publisher: Elsevier Science B.V..

AB This paper describes a procedure in which **cysteine** contg. **peptides** from tryptic **digests** of complex protein mixts. were selected by covalent chromatog. based on thiol-**disulfide** exchange, identified by **mass spectrometry**, and quantified by differential **isotope** labeling. Following disruption of **disulfide** bridges with 2,2'-dipyridyl **disulfide**, all proteins were **digested** with **trypsin** and acylated with succinic anhydride. **Cysteine** contg. **peptides** were then selected from the acylated **digest** by **disulfide** interchange

★ Similar but no ALICE (comps.)

with sulfhydryl groups on a thiopropyl Sepharose gel. Captured **cysteine** contg. **peptides** were released from the gel with 25 mM dithiothreitol (pH 7.5) contg. 1 mM (ethylenedinitrilo)tetraacetic acid disodium salt and alkylated with iodoacetic acid subsequent to fractionation by reversed-phase liq. chromatog. (RPLC). Fractions collected from the RPLC column were analyzed by matrix-assisted laser desorption ionization **mass spectrometry**. Based on **isotope** ratios of **peptides** from exptl. and control samples labeled with succinic and **deuterated** succinic anhydride, resp., it was possible to det. the relative concn. of each **peptide** species between the two samples. **Peptides** obtained from proteins that were up-regulated in the exptl. sample were easily identified by an increase of the relative amt. of the **deuterated peptide**. The results of these studies indicate that by selecting **cysteine** contg. **peptides**, the complexity of protein **digest** could be reduced and database searches greatly simplified. When coupled with the **isotope** labeling strategy for quantification it was possible to **det. proteins** that were up-regulated in plasmid bearing Escherichia coli when expression of plasmid proteins was induced. Up-regulation of several proteins of E. coli origin was also noted.

CC 9-16 (Biochemical Methods)
ST proteome detection covalent chromatog MALDI **mass spectrometry**

IT Chromatography
(covalent; proteomics based on selecting and quantifying **cysteine** contg. **peptides** by covalent chromatog.)

IT Laser ionization **mass spectrometry**
(photodesorption, matrix-assisted; proteomics based on selecting and quantifying **cysteine** contg. **peptides** by covalent chromatog.)

IT Laser desorption **mass spectrometry**
(photoionization, matrix-assisted; proteomics based on selecting and quantifying **cysteine** contg. **peptides** by covalent chromatog.)

IT Databases
Escherichia coli
Reversed phase liquid chromatography
Sulfhydryl group
(proteomics based on selecting and quantifying **cysteine** contg. **peptides** by covalent chromatog.)

IT **Proteins, general, analysis**
(proteomics based on selecting and quantifying **cysteine** contg. **peptides** by covalent chromatog.)

IT 484-42-4 9001-63-2, Lysozyme 71800-36-7, 1-9-Kallidin

75909-25-0 76310-14-0, 1-6-Adrenorphin (human) 117620-76-5
359706-65-3 359706-67-5

(proteomics based on selecting and quantifying **cysteine**
contg. **peptides** by covalent chromatog.)

IT 2127-03-9, 2,2'-Dipyridyl **disulfide**
(proteomics based on selecting and quantifying **cysteine**
contg. **peptides** by covalent chromatog.)

L98 ANSWER 15 OF 28 HCA COPYRIGHT 2004 ACS on STN

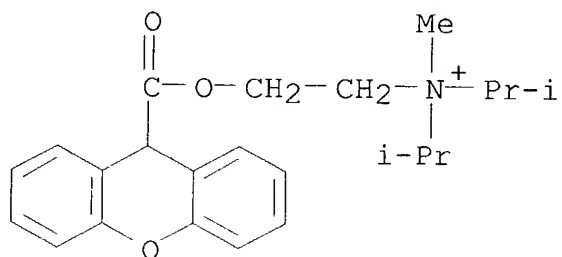
134:362292 Methods of determining individual hypersensitivity to a
pharmaceutical agent from gene expression profile. Farr, Spencer
(Phase-1 Molecular Toxicology, USA). PCT Int. Appl. WO 2001032928
A2 20010510, 222 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ,
EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG,
KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX,
MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ,
TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR,
GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR.
(English). CODEN: PIXXD2. APPLICATION: WO 2000-US30474 20001103.
PRIORITY: US 1999-PV165398 19991105; US 2000-PV196571 20000411.

AB The invention discloses methods, gene databases, gene arrays,
protein arrays, and devices that may be used to det. the
hypersensitivity of individuals to a given agent, such as drug or
other chem., in order to prevent toxic side effects. In one
embodiment, methods of identifying hypersensitivity in a subject by
obtaining a gene expression profile of multiple genes assocd. with
hypersensitivity of the subject suspected to be hypersensitive, and
identifying in the gene expression profile of the subject a pattern
of gene expression of the genes assocd. with hypersensitivity are
disclosed. The gene expression profile of the subject may be
compared with the gene expression profile of a normal individual and
a hypersensitive individual. The gene expression profile of the
subject that is obtained may comprise a profile of levels of mRNA or
cDNA. The gene expression profile may be obtained by using an array
of nucleic acid probes for the plurality of genes assocd. with
hypersensitivity. The expression of the genes predetd. to be
assocd. with hypersensitivity is directly related to prevention or
repair of toxic damage at the tissue, organ or system level. Gene
databases arrays and app. useful for identifying hypersensitivity in
a subject are also disclosed.

IT 298-50-0, Propantheline
(methods of detg. individual hypersensitivity to a pharmaceutical
agent from gene expression profile)

RN 298-50-0 HCA

CN 2-Propanaminium, N-methyl-N-(1-methylethyl)-N-[2-[(9H-xanthen-9-
ylcarbonyl)oxy]ethyl]- (9CI) (CA INDEX NAME)



- IC ICM C12Q001-68
ICS G01N033-50
- CC 3-4 (Biochemical Genetics)
Section cross-reference(s): 1, 6, 7, 13, 15
- IT Multidrug resistance proteins
(BCRP (breast cancer resistance **protein**); methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Glycoproteins, specific or class
(C4bp (complement C4b-binding **protein**); methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class
(CAP (adenylate cyclase-assocd. **protein**); methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Gene, animal
(G/T mismatch binding **protein**; methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Cyclins
(G1, cyclin G1 interacting **protein**; methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class
(GT mismatch binding **protein**; methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class
(L-FABP (liver fatty acid-binding **protein**); methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Cytokines
(MBP (major basic **protein**); methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class

- (Nucleosome assembly **protein**; methods of **detg**
. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class
(PABP (poly(A)-binding **protein**); methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class
(PDGF assocd. **protein**; methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class
(c-myc binding **protein**; methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Gene, animal
(lipopolysaccharide binding **protein**; methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT APC **protein**
(methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Mdm2 **protein**
(methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Multidrug resistance **proteins**
(methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Myelin basic **protein**
(methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Prion **proteins**
(methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT p53 (**protein**)
(methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Gene, animal
(myelin basic **protein**; methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Gene, animal
(nucleic acid binding **protein**; methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene expression profile)
- IT Proteins, specific or class
(oxysterol binding **protein**; methods of **detg**. individual hypersensitivity to a pharmaceutical agent from gene

- expression profile)
- IT Proteins, specific or class
(pancreatitis-assocd. **protein**; methods of **detg**
. individual hypersensitivity to a pharmaceutical agent from gene
expression profile)
- IT Proteins, general, biological studies
(**proteinuria**; methods of **detg**. individual
hypersensitivity to a pharmaceutical agent from gene expression
profile)
- IT Proteins, specific or class
(thiol-specific antioxidant **protein**; methods of
detg. individual hypersensitivity to a pharmaceutical
agent from gene expression profile)
- IT Proteins, specific or class
(ts11 gene encoding G1 progression **protein**; methods of
detg. individual hypersensitivity to a pharmaceutical
agent from gene expression profile)
- IT 50-02-2, Dexamethasone 50-06-6, Phenobarbital, biological studies
50-18-0, Cyclophosphamide 50-23-7, Hydrocortisone 50-24-8,
Prednisolone 50-28-2, Estradiol, biological studies 50-44-2,
6-Thiopurine 50-48-6, Amitriptyline 50-55-5, Reserpine
50-76-0, Actinomycin D 50-78-2, Aspirin 51-06-9, Procainamide
51-21-8, Fluorouracil 51-34-3, Scopolamine 51-48-9,
Levothyroxine, biological studies 51-49-0, Dextrothyroxine
51-55-8, Atropine, biological studies 51-75-2, Mechlorethamine
52-01-7, Spironolactone 52-53-9, Verapamil 52-67-5,
Penicillamine 52-86-8, Haloperidol 53-03-2, Prednisone
53-06-5, Cortisone 53-19-0, Mitotane 53-33-8, Paramethasone
53-86-1, Indomethacin 54-05-7, Chloroquine 54-11-5, Nicotine
54-31-9, Furosemide 54-36-4, Metyrapone 54-85-3, Isoniazid
55-63-0, Nitroglycerin 55-65-2, Guanethidine 55-98-1, Busulfan
56-54-2, Quinidine 56-75-7, Chloramphenicol 57-22-7, Vincristine
57-41-0, Phenytoin 57-53-4, Meprobamate 57-63-6, Ethinyl
estradiol 57-66-9, Probenecid 57-83-0, Progestin, biological
studies 57-96-5, Sulfinpyrazone 58-05-9, Leucovorin 58-14-0,
Pyrimethamine 58-32-2, Dipyridamole 58-39-9, Perphenazine
58-54-8, Ethacrynic acid 58-55-9, Theophylline, biological studies
58-61-7, Adenosine, biological studies 58-74-2, Papaverine
58-93-5, Hydrochlorothiazide 58-94-6, Thiazide 59-05-2,
Methotrexate 59-42-7, Phenylephrine 59-43-8, Thiamine,
biological studies 59-92-7, Levodopa, biological studies
59-99-4, Neostigmine 60-40-2, Mecamylamine 60-54-8, Tetracycline
60-79-7, Ergonovine 60-87-7, Promethazine 61-32-5, Methicillin
61-72-3, Cloxacillin 64-75-5, Tetracycline hydrochloride
64-77-7, Tolbutamide 64-86-8, Colchicine 65-23-6, Pyridoxine
66-79-5, Oxacillin 66-97-7, Psoralen 67-20-9, Nitrofurantoin
67-45-8, Furazolidone 67-68-5, Dimethyl sulfoxide, biological
studies 68-22-4D, Norethindrone, mixt. with ethinyl estradiol

68-41-7, Cycloserine 68-88-2, Hydroxyzine 69-53-4, Ampicillin
69-72-7, biological studies 69-89-6, Xanthine 73-24-5,
6-Aminopurine, biological studies 73-31-4, Melatonin 76-42-6,
Oxycodone 76-57-3, Codeine 77-09-8, Phenolphthalein 77-19-0,
Dicyclomine 77-36-1, Chlorthalidone 78-44-4, Carisoprodol
80-08-0, Dapsone 81-23-2, Dehydrocholic acid 81-81-2, Warfarin
82-92-8, Cyclizine 82-95-1, Buclizine 83-43-2,
Methylprednisolone 83-73-8, Iodoquinol 83-89-6, Quinacrine
83-98-7, Orphenadrine 86-54-4, Hydralazine 89-57-6, Mesalamine
90-34-6, Primaquine 90-82-4, Pseudoephedrine 91-64-5, Coumarin
92-13-7, Pilocarpine 92-84-2, Phenothiazine 93-14-1, Guaifenesin
94-20-2, Chlorpropamide 94-36-0, Benzoyl peroxide, biological
studies 94-78-0, Phenazopyridine 95-25-0, Chlorzoxazone
96-64-0, Soman 97-77-8, Disulfiram 99-66-1, Valproic acid
100-33-4, Pentamidine 100-97-0, Methenamine, biological studies
101-31-5, Hyoscyamine 103-90-2, Acetaminophen 113-18-8,
Ethchlorvynol 113-42-8, Methylergonovine 113-45-1,
Methylphenidate 114-07-8, Erythromycin 114-86-3, Phenformin
118-42-3, Hydroxychloroquine 122-09-8, Phentermine 123-56-8,
Succinimide 123-63-7, Paraldehyde 124-94-7, Triamcinolone
125-29-1, Hydrocodone 125-33-7, Primidone 125-64-4, Methyprylon
125-71-3, Dextromethorphan 125-84-8, Aminoglutethimide 126-07-8,
Griseofulvin 126-52-3, Ethinamate 127-07-1, Hydroxyurea
127-69-5, Sulfisoxazole 128-13-2, Ursodiol 130-95-0, Quinine
132-17-2, Benztropine 133-10-8, Sodium p-aminosalicylate
137-58-6, Lidocaine 138-56-7, Trimethobenzamide 144-11-6,
Trihexyphenidyl 147-52-4, Nafcillin 147-94-4, AraC 148-82-3,
Melfalan 154-21-2, Lincomycin 154-42-7, Thioguanine 154-93-8,
Carmustine 155-97-5, Pyridostigmine 298-46-4,
5H-Dibenz[b,f]azepine-5-carboxamide 298-50-0,
Propantheline 299-42-3, Ephedrine 300-62-9D, Amphetamine, mixed
300-62-9D, Amphetamine, mixed salts 302-17-0, Chloral hydrate
302-79-4, Tretinoin 303-53-7, Cyclobenzaprine 305-03-3,
Chlorambucil 315-30-0, Allopurinol 321-64-2, Tacrine 346-18-9,
Polythiazide 361-37-5, Methysergide 363-24-6, Dinoprostone
364-62-5, Metoclopramide 378-44-9, Betamethasone 389-08-2,
Nalidixic acid 395-28-8, Isoxsuprine 439-14-5, Diazepam
443-48-1, Metronidazole 446-86-6, Azathioprine 456-59-7,
Cyclandelate 461-72-3, Hydantoin 463-04-7, Amyl nitrite
469-62-5, Propoxyphene 474-25-9, Chenodiol 480-30-8,
Dichloralphenazone 484-23-1, Dihydralazine 503-01-5,
Isometheptene 512-15-2, Cyclopentolate 520-85-4,
Medroxyprogesterone 525-66-6, Propranolol 526-36-3,
Xylometazoline 536-33-4, Ethionamide 541-15-1, Levocarnitine
546-88-3, Acetohydroxamic acid 555-30-6, Methyl dopa 564-25-0,
Doxycycline 569-65-3, Meclizine 577-11-7, Docusate sodium
596-51-0, Glycopyrrolate 599-79-1, Sulfasalazine 603-50-9,
Bisacodyl 634-03-7, Phendimetrazine 637-07-0, Clofibrate

657-24-9, Metformin 671-16-9, Procarbazine 672-87-7, Metyrosine
 674-38-4, Bethanechol 723-46-6, Sulfamethoxazole 738-70-5,
 Trimethoprim 745-65-3, Alprostadil 791-35-5, Chlophedianol
 797-63-7, Levonorgestrel 797-64-8D, L-Norgestrel, ethinyl
 estradiol mixt. 846-49-1, Lorazepam 846-50-4, Temazepam
 911-45-5, Clomiphene 915-30-0, Diphenoxylate 962-58-3, Diazoxon
 968-93-4, Testolactone 972-02-1, Diphenidol 990-73-8, Fentanyl
 citrate 1134-47-0, Baclofen 1143-38-0, Anthralin 1321-13-7,
 Potassium aminobenzoate 1397-89-3, Amphotericin B 1400-61-9,
 Nystatin 1404-04-2, Neomycin 1404-04-2D, Neomycin, mixt. with
 polymx/HC 1404-90-6, Vancomycin 1406-05-9, Penicillin
 1491-59-4, Oxymetazoline 1622-61-3, Clonazepam 1953-02-2,
 Tiopronin 1977-10-2, Loxapine 2152-34-3, Pemoline 2152-44-5,
 Betamethasone valerate 2447-57-6, Sulfadoxine 2451-01-6, Terpin
 hydrate 2609-46-3, Amiloride 2809-21-4 2998-57-4, Estramustine
 3116-76-5, Dicloxacillin 3313-26-6, Thiothixene 3385-03-3,
 Flunisolide 3485-14-1, Cyclacillin 3737-09-5, Disopyramide
 3778-73-2, Iphosphamide 3930-20-9, Sotalol 4205-90-7, Clonidine
 4419-39-0, Beclomethasone

(methods of detg. individual hypersensitivity to a pharmaceutical
 agent from gene expression profile)

IT 107-97-1, Sarcosin 447-41-6, Nylidrin 8056-51-7 9000-86-6,
 Alanine aminotransferase 9000-97-9 9001-05-2, Catalase
 9001-40-5, Glucose-6-phosphate dehydrogenase 9001-48-3,
 Glutathione reductase 9001-50-7, Glyceraldehyde 3-phosphate
 dehydrogenase 9001-62-1, Hepatic lipase 9001-84-7, Phospholipase
 A2 9002-03-3, Dihydrofolate reductase 9002-06-6, Thymidine
 kinase 9002-12-4, Urate oxidase 9002-67-9, Luteinizing hormone
 9003-99-0, Myeloperoxidase 9012-25-3, Catechol-O-methyltransferase
 9012-38-8, PAPS synthetase 9012-39-9 9012-52-6,
 S-Adenosylmethionine synthetase 9013-08-5, Phosphoenolpyruvate
 carboxykinase 9013-18-7, Fatty acyl-CoA synthetase 9013-38-1,
 Dopamine .beta.-hydroxylase 9013-66-5, Glutathione peroxidase
 9013-79-0, Neuropathy target esterase 9014-55-5, Tyrosine
 aminotransferase 9015-71-8, Corticotropin releasing hormone
 9015-81-0, 17-.beta. Hydroxysteroid dehydrogenase 9016-12-0,
 Hypoxanthine-guanine phosphoribosyltransferase 9023-44-3,
 Tryptophanyl-tRNA synthetase 9023-62-5, Glutathione synthetase
 9023-64-7, .gamma.-Glutamylcysteinyl synthetase 9023-70-5,
 Glutamine synthetase 9024-60-6, Ornithine decarboxylase
 9024-61-7, Histidine decarboxylase 9025-32-5, Prolidase
 9026-00-0, Cholesterol esterase 9026-09-9, Phenol sulfotransferase
 9026-43-1, Serine kinase 9026-51-1, Nucleoside diphosphate kinase
 9027-13-8, Enoyl-CoA hydratase 9027-65-0, Acyl-CoA dehydrogenase
 9028-06-2 9028-31-3, Aldose reductase 9028-35-7, HMG CoA
 reductase 9028-41-5, Hydroxyacyl-Coenzyme A dehydrogenase
 9028-86-8, Aldehyde dehydrogenase 9029-73-6, Phenyl alanine
 hydroxylase 9029-80-5, Histamine N-methyltransferase 9029-97-4,

3-Ketoacyl-CoA thiolase 9031-37-2, Ceruloplasmin 9031-54-3,
 Sphingomyelinase 9031-61-2, Thymidylate synthase 9031-72-5,
 Alcohol dehydrogenase 9032-20-6, DT-Diaphorase 9035-58-9,
 Blood-coagulation factor III 9036-22-0, Tyrosine hydroxylase
 9037-21-2, Tryptophan hydroxylase 9037-62-1, Glycyl tRNA
 synthetase 9039-06-9, NADPH cytochrome P450 reductase 9040-57-7,
 Ribonucleotide reductase 9041-92-3 9045-77-6, Fatty acid
 synthase 9046-27-9, .gamma.-Glutamyl transpeptidase 9048-63-9,
 Epoxide hydrolase 9055-67-8, Poly(ADP-ribose)polymerase
 9059-25-0, Lysyl oxidase 9068-41-1, Carnitine palmitoyltransferase
 9074-02-6, Malic enzyme 9074-10-6, Biliverdin reductase
 9074-19-5, Hydratase 9074-87-7, .gamma.-Glutamyl hydrolase
 9081-36-1, 25-Hydroxyvitamin D3 1-hydroxylase 11096-26-7,
 Erythropoietin 37205-63-3, ATP synthase 37237-44-8,
 Glucosylceramide synthase 37289-06-8, Acid ceramidase
 37292-81-2, Cytochrome p.450 11A1 37318-49-3, Protein
disulfide isomerase 39391-18-9, Prostaglandin H synthase
 52228-01-0 56093-23-3, .alpha.-1,2-Fucosyl transferase
 56645-49-9, Cathepsin G 59536-73-1, Phosphomannomutase
 59536-74-2, Very long-chain acyl-CoA dehydrogenase 60267-61-0,
 Ubiquitin 60616-82-2, Cathepsin L 61116-22-1, Fatty acyl-CoA
 oxidase 62229-50-9, Epidermal growth factor 67339-09-7,
 Thiopurine methyltransferase 67763-96-6, Insulin-like growth
 factor 1 67763-97-7, Insulin-like growth factor II 77271-19-3,
 6-O-Methylguanine-DNA methyltransferase 77847-96-2,
 Prostacyclin-stimulating factor 79747-53-8, Protein tyrosine
 phosphatase 79955-99-0, Stromelysin-1 80146-85-6, Tissue
 Transglutaminase 80295-41-6, Complement component C3 81627-83-0,
 Colony stimulating factor -1 82391-43-3, 12-Lipoxygenase
 83268-44-4 83869-56-1, Granulocyte-macrophage colony-stimulating
 factor 85637-73-6, Atrial natriuretic factor 87397-91-9,
 Thymosin .beta.10 88943-21-9, Proteinase .alpha.1-inhibitor III
 89964-14-7, Prothymosin, alpha 90698-26-3, Ribosomal protein S6
 kinase 96024-44-1, Granulin 105238-46-8, Macropain
 106096-92-8, Fibroblast growth factor, acidic 106956-32-5,
 Oncostatin M 112130-98-0, Procathepsin L 114949-22-3, Activin (
protein) 117698-12-1, Paraoxonase 119418-04-1, Galanin
 122191-40-6, Caspase-1 123626-67-5, Endothelin-1 125978-95-2,
 Nitric oxide synthase 127464-60-2, Vascular endothelial growth
 factor 137632-07-6, Extracellular-signal-regulated kinase 1
 138238-81-0, Endothelin converting enzyme-1 140208-24-8, Tissue
 inhibitor of metalloproteinase-1 141176-92-3 141349-86-2, Cyclin
 dependent kinase 2 141436-78-4, Protein kinase C 142243-03-6,
 Plasminogen activator inhibitor 2 142805-56-9, DNA topoisomerase
 II 142805-58-1, MAP kinase kinase 143180-75-0, DNA topoisomerase
 I 143375-65-9, Cyclin dependent kinase 1 145809-21-8, Tissue
 inhibitor of metalloproteinase-3 146480-35-5, Matrix
 metalloproteinase-2 147014-97-9, Cyclin dependent kinase 4

148348-15-6, Fibroblast growth factor 7 149316-81-4, Branched chain acyl-CoA oxidase 149371-05-1, Kinase (phosphorylating), gene c-abl **protein** 149885-78-9, Hepatocyte growth factor activator 154907-65-0, Checkpoint kinase 155807-64-0, FEN-1 Endonuclease 165245-96-5, p38 Mitogen-activated protein kinase 169592-56-7, CPP32 **proteinase** 179241-70-4, Protein kinase ZPK 179241-78-2, Caspase 8 182372-14-1, Caspase 2 182372-15-2, Caspase 6 182762-08-9, Caspase 4 189258-14-8, Caspase 7 192465-11-5, Caspase 5 193363-12-1, Vascular endothelial growth factor D 194554-71-7, Tissue factor pathway inhibitor 205944-50-9, Osteoprotegerin 220983-94-8, Sorbitol dehydrogenase 289898-51-7, JNK1 protein kinase 303752-61-6, DNA dependent protein kinase 329736-03-0, Cytochrome p450 3A4 329764-85-4, Cytochrome p450 1A1 329900-75-6, Cyclooxygenase 2 329978-01-0, Cytochrome p450 2C9 330196-64-0, Cytochrome p450 1A2 330196-93-5, Cytochrome p450 2E1 330207-10-8, Cytochrome p450 2B1 330589-90-7, Cytochrome p450 2C19 330596-22-0, Cytochrome p450 1B1 330597-62-1, Cytochrome p450 2D6 330975-22-9, Macrostatin 331462-97-6, Cytochrome p450 2B2 331462-98-7, Cytochrome p450 3A1 331823-00-8, Cytochrome p450 2C11 331823-12-2, Cytochrome p450 2C12 331823-27-9, Cytochrome p450 2A1 331827-06-6, Cytochrome p450 2A6 332847-52-6, Cytochrome p450 4A 336884-26-5, Cytochrome p450 2B10 338964-08-2, P 450 17A 338969-62-3, P 450 2A3 338969-69-0, P 450 2F2 338969-71-4, P 450 4A1
 (methods of **detg.** individual hypersensitivity to a pharmaceutical agent from gene expression profile)

L98 ANSWER 16 OF 28 HCA COPYRIGHT 2004 ACS on STN

131:269143 Dynamic measurement of myosin light-chain-domain tilt and twist in muscle contraction. Corrie, J. E. T.; Brandmeier, B. D.; Ferguson, R. E.; Trentham, D. R.; Kendrick-Jones, J.; Hopkins, S. C.; Van Der Heide, U. A.; Goldman, Y. E.; Sabido-David, C.; Dale, R. E.; Criddle, S.; Irving, M. (National Institute for Medical Research, London, NW7 1AA, UK). Nature (London), 400(6743), 425-430 (English) 1999. CODEN: NATUAS. ISSN: 0028-0836. Publisher: Macmillan Magazines.

AB A new method is described for **measuring** motions of **protein** domains in their native environment on the physiol. timescale. Pairs of **cysteines** are introduced into the domain at sites chosen from its static structure and are crosslinked by a bifunctional rhodamine. Domain orientation in a reconstituted macromol. complex is detd. by combining fluorescence polarization data from a small no. of such labeled **cysteine** pairs. This approach bridges the gap between in vitro studies of **protein** structure and cellular studies of **protein** function and is used here to measure the tilt and twist of the myosin light-chain domain with respect to actin filaments in single muscle cells. The results reveal the structural basis for the

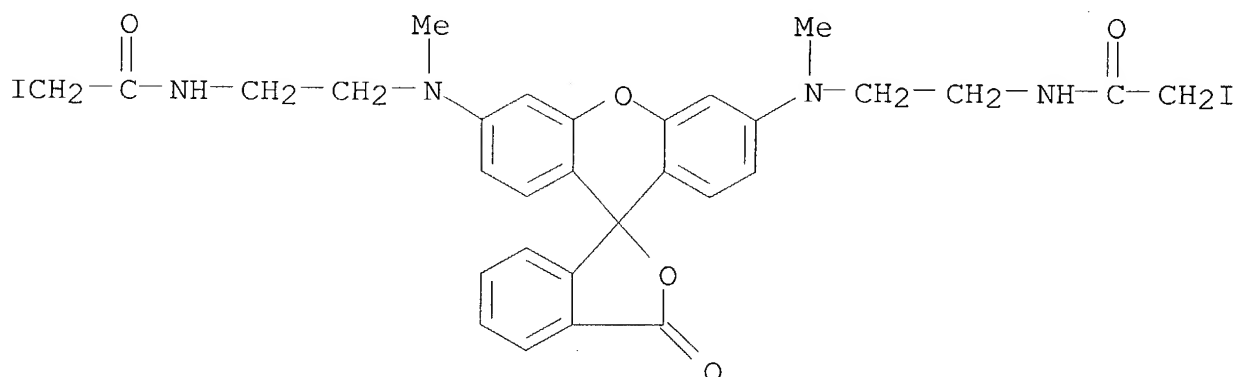
lever-arm action of the light-chain domain of the myosin motor during force generation in muscle.

IT 203580-70-5

(bifunctional rhodamine label for myosin light-chain-domain; dynamic measurement of myosin light-chain-domain tilt and twist in muscle contraction)

RN 203580-70-5 HCA

CN Acetamide, N,N'-[(3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthene]-3',6'-diyl)bis[(methylimino)-2,1-ethanediyl]]bis[2-iodo- (9CI) (CA INDEX NAME)



CC 9-5 (Biochemical Methods)
Section cross-reference(s): 6, 13

IT Quaternary structure
(**protein**; dynamic **measurement** of myosin light-chain-domain tilt and twist in muscle contraction)

IT 203580-70-5

(bifunctional rhodamine label for myosin light-chain-domain; dynamic measurement of myosin light-chain-domain tilt and twist in muscle contraction)

L98 ANSWER 17 OF 28 HCA COPYRIGHT 2004 ACS on STN

131:167851 Purification, structural characterization, cloning and immunocytochemical localization of chemoreception proteins from *Schistocerca gregaria*. Angeli, Sergio; Ceron, Francesca; Scaloni, Andrea; Monti, Maria; Monteforti, Gaia; Minnocci, Antonio; Petacchi, Ruggero; Pelosi, Paolo (Scuola Superiore di Studi Universitari e di Perfezionamento "S. Anna", Pisa, Italy). *European Journal of Biochemistry*, 262(3), 745-754 (English) 1999. CODEN: EJBCAI. ISSN: 0014-2956. Publisher: Blackwell Science Ltd..

AB Sol. low-mol.-mass protein isoforms were purified from chemosensory organs (antennae, tarsi, and labrum) of the desert locust *S. gregaria*. Five genes encoding proteins of this group were amplified by PCR from cDNAs of tarsi and sequenced. Their expression products are **polypeptide** chains of 109 amino acids showing 40-50%

sequence identity with putative olfactory proteins from *Drosophila melanogaster* and *Cactoblastis cactorum*. Direct structural investigation on isoforms purified from chemosensory organs revealed the presence in the expression products of two of the genes cloned. Two addnl. **protein** isoforms were **detected** and their mol. structure exhaustively characterized. MS anal. of all isoforms demonstrated that the 4 **cysteine** residues conserved in the **polypeptide** chain were involved in **disulfide** bridges (Cys29-Cys38 and Cys57-Cys60) and indicated the absence of any addnl. post-translational modifications. Immunocytochem. expts., performed with rabbit antiserum raised against the protein isoform mixt., showed selective labeling of the outer lymph in contact sensilla of tarsi, maxillary palps, and antennae. Other types of sensilla were not labeled, nor were the cuticle and dendrites of the sensory cells. No binding of **radioactively labeled** glucose or bicarbonate was detected, in disagreement with the hypothesis that this class of proteins is involved in the CO₂-sensing cascade. Our exptl. data suggest that the proteins described here could be involved in contact chemoreception in Orthoptera.

CC 12-1 (Nonmammalian Biochemistry)
Section cross-reference(s): 3, 6

L98 ANSWER 18 OF 28 HCA COPYRIGHT 2004 ACS on STN

131:56155 Methods for the simultaneous identification of novel biological targets and lead structures for drug development using combinatorial libraries and probes. Heefner, Donald L.; Zepp, Charles M.; Gao, Yun; Jones, Steven W. (Sepracor Inc., USA). PCT Int. Appl. WO 9931267 A1 19990624, 125 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO 1998-US26894 19981218. PRIORITY: US 1997-68035 19971218.

AB The combinatorial screening assays and detection methods of the present invention encompass highly diversified libraries of compds. which act as fingerprints to allow for the identification of specific mol. differences existing between biol. samples. The combinatorial screening assay and detection methods of the present invention utilize highly diversified libraries of compds. to interrogate and characterize complex mixts. in order to identify specific mol. differences existing between biol. samples, which may serve as targets for diagnosis of development of therapeutics. The invention is base, in part, on the design of sensitive, rapid,

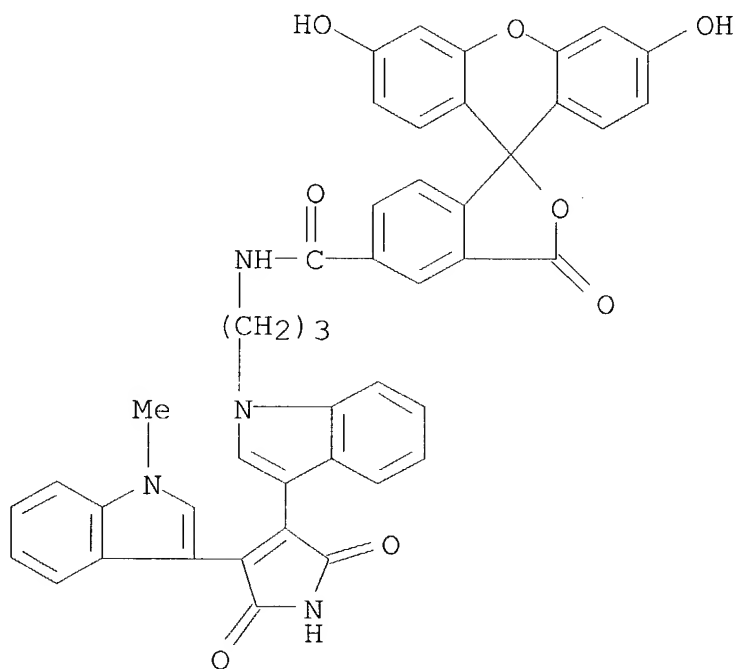
homogeneous assay systems that permit the evaluation, interrogation, and characterization of samples using complex, highly diversified libraries of mol. probes. The ability to run the high throughput assays in a homogeneous format increases sensitivity of screening. In addn., the homogeneous format allows the mols. which interact to maintain their native or active conformations. Moreover, the homogeneous assay systems of the invention utilize robust detection systems that do not require sepn. steps for detection of reaction products. The assays of the invention can be used for diagnostics, drug screening and discovery, target-driven discover, and in the field of proteomics and genomics for the identification of disease markers and drug targets.

IT 220518-50-3, Fim-1

(identification of novel biol. targets and lead structures for drug development using combinatorial libraries and probes)

RN 220518-50-3 HCA

CN Spiro[isobenzofuran-1(3H),9']-[9H]xanthene]-5-carboxamide, N-[3-[3-[2,5-dihydro-4-(1-methyl-1H-indol-3-yl)-2,5-dioxo-1H-pyrrol-3-yl]-1H-indol-1-yl]propyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)



IC ICM C12Q001-00

ICS C12Q001-68; C12Q001-70; G01N033-53; G01N033-566; G01N033-567; G01N021-00; G01N021-76

CC 9-16 (Biochemical Methods)

Section cross-reference(s): 1, 6, 13, 14

IT Animal tissue
 Autoimmune disease
 Biochemical molecules
 Blood
 Blood analysis
 Blood plasma
 Blood serum
 Body fluid
 Cell
 Chemiluminescence spectroscopy
 Chemiluminescent substances
 Chicken (Gallus domesticus)
 Combinatorial chemistry
 Combinatorial library
 Crosslinking
 Diabetes mellitus
 Diagnosis
 Disease, animal
 Drug design
 Drug screening
 Drugs
 Epitopes
 Erythrocyte
 Escherichia coli
 Fluorescent dyes
 Fluorescent probes
 Fluorescent substances
 Fluorometry
 Heart, disease
 Immobilization, biochemical
 Infection
 Inflammation
 Leukocyte
 Lymph
 Microorganism
 Molecules
 Neoplasm
 Photochemistry
 Polarized fluorescence
 Radioactive substances
 Scintillators
 Test kits
 Therapy
 Toxicity
 Urine
 Urine analysis
 Virus
 (identification of novel biol. targets and lead structures for

- drug development using combinatorial libraries and probes)
- IT Amino acids, analysis
Antibodies
Antigens
Carbohydrates, analysis
Chemokines
Cytokines
DNA
Enzymes, analysis
Glycolipids
 Glycoproteins, general, analysis
Growth factors, animal
Inorganic compounds
Ligands
Lipids, analysis
Lipopolysaccharides
 Lipoproteins
Nucleosides, analysis
Nucleotides, analysis
Oligonucleotides
Oligosaccharides, analysis
Organic compounds, analysis
Peptides, analysis
Polymers, analysis
Polynucleotides
Polysaccharides, analysis
 Proteins, general, analysis
RNA
Receptors
 (identification of novel biol. targets and lead structures for
 drug development using combinatorial libraries and probes)
- IT 50-06-6D, Phenobarbital, reaction products with fluorescein
50-67-9D, Serotonin, reaction products with coumarin, analysis
57-41-0D, Phenytoin, reaction products with fluorescein 58-55-9D,
Theophylline, reaction products with fluorescein 70-51-9D,
Desferrioxamine, reaction products with fluorescein 125-33-7D,
Primidone, reaction products with fluorescein 536-21-0D,
Norphenylephrine, reaction products with coumarin 1403-66-3D,
Gentamicin, reaction products with fluorescein 1404-90-6D,
Vancomycin, reaction products with fluorescein 1446-61-3D,
Dehydroabietylamine, reaction products with fluorescein and coumarin
6621-47-2D, Perhexiline, reaction products with fluorescein
11032-79-4D, .alpha.-Bungarotoxin, reaction products with FITC
20350-15-6D, Brefeldin A, reaction products with BODIPY
32231-06-4D, 1-Piperonylpiperazine, reaction products with
fluorescein and coumarin 32795-44-1D, N-Acetylprocainamide,
reaction products with fluorescein 32986-56-4D, Tobramycin,
reaction products with fluorescein 37517-28-5D, Amikacin, reaction

products with fluorescein 66580-68-5D, Globotriose, reaction
 products with fluorescein 70458-96-7D, Norfloxacin, reaction
 products with coumarin 74011-58-8D, Enoxacin, reaction products
 with coumarin 84031-84-5, Colchicine fluorescein 87134-87-0
 88641-41-2, Naloxone fluorescein 88641-43-4 107827-77-0
 121086-10-0, BODIPY FL-NAPS 121714-22-5, Fluo-3AM 134759-22-1,
 Fluorescein biotin 135243-34-4, BODIPY FL PPHT 137759-83-2
 138777-24-9, C 8FDG 151736-99-1, Cholesteryl-BODIPY FL C12
 168004-84-0 170516-42-4, Phen Green 175799-93-6, BODIPY
 FL-prazosin 195244-55-4, Sodium Green 197460-05-2, Fluorescein
 methotrexate 212116-60-4, BODIPY FL-forskolin 216483-91-9, Ro
 1986-BODIPY 216483-92-0, BODIPY FL-amiloride 216571-97-0, BODIPY
 FL-ABT 216571-98-1, BODIPY FL-bisindolylmaleimide 216571-99-2,
 BODIPY FL-thapsigargin 216572-00-8, BODIPY FL-X ryanodine
 216854-76-1, Dexamethasone fluorescein 217189-42-9, (+)-DM-BODIPY
 dihydropyridine 217189-43-0, (-)-DM-BODIPY dihydropyridine
 217189-44-1, BODIPY FL C12-galactocerebroside **220518-50-3**,
 Fim-1 228111-69-1 228111-70-4 228111-71-5 228262-70-2,
 Fluorescein DHPE 228265-61-0, BODIPY FL pirenzepine 228265-62-1,
 BODIPY FL-CGP 12177 228265-63-2, BODIPY FL C12-MPP 228265-94-9,
 BODIPY FL-Sch 23390 288374-37-8, Newport Green

(identification of novel biol. targets and lead structures for
 drug development using combinatorial libraries and probes)

L98 ANSWER 19 OF 28 HCA COPYRIGHT 2004 ACS on STN

130:308804 Target protein sequences for binding of synthetic biarsenical
 molecules. Tsien, Roger Y.; Griffin, Albert B. (The Regents of the
 University of California, USA). PCT Int. Appl. WO 9921013 A1
 19990429, 77 pp. DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB,
 BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM,
 HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
 LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
 SK, SL, TJ, TM, TR, TT, UA, UG, US, US, US, UZ, VN, YU, ZW, AM, AZ,
 BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM,
 CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL,
 PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO
 1998-US22363 19981021. PRIORITY: US 1997-955050 19971021; US
 1997-955206 19971021; US 1997-955859 19971021.

AB The present invention features biarsenical mols. and target
 sequences that specifically react with the biarsenical mols. A
 bonding partner comprises a carrier polypeptide and a target
 sequence, wherein the target sequence is heterologous to the carrier
 polypeptide and the target sequence contains one or more
cysteines capable of specifically reacting with a
 biarsenical mol. Bonding partners that include target sequences,
 vectors that include nucleic acid sequences that encode the target
 sequences and host cells that include the target sequences are also
 featured in the invention. One example of a biarsenical compd. is

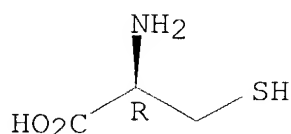
an arsenical deriv. of fluorescein.

IT 52-90-4, L-Cysteine, biological studies
(target protein sequences for binding of synthetic biarsenical
mols.)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.

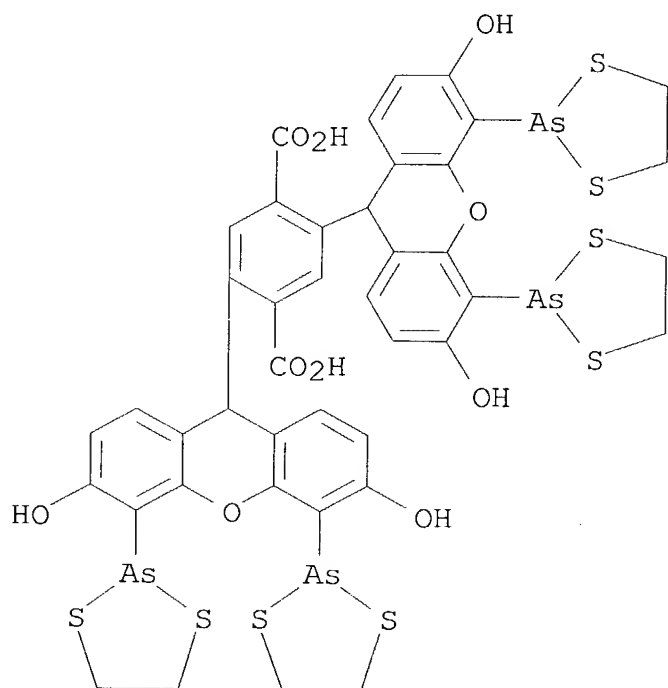


IT 223673-80-1 223673-81-2 223673-82-3

(target protein sequences for binding of synthetic biarsenical
mols.)

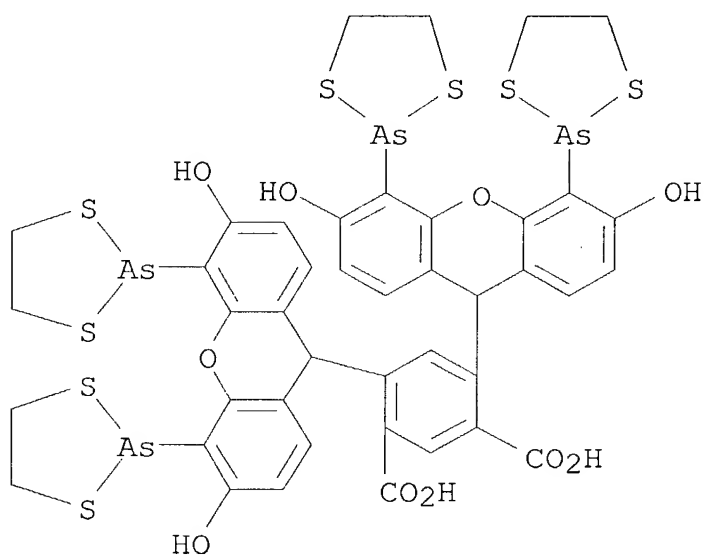
RN 223673-80-1 HCA

CN 1,4-Benzenedicarboxylic acid, 2,5-bis[4,5-bis(1,3,2-dithiarsolan-2-yl)-3,6-dihydroxy-9H-xanthen-9-yl]- (9CI) (CA INDEX NAME)



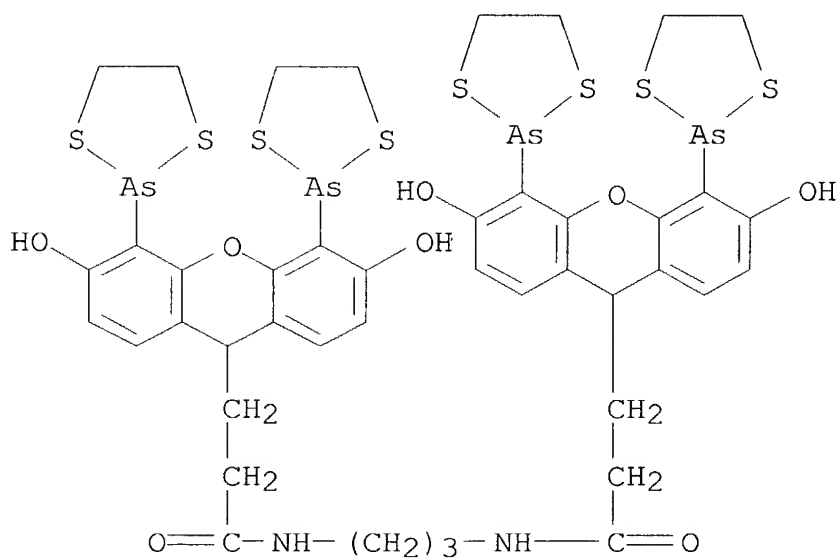
RN 223673-81-2 HCA

CN 1,3-Benzenedicarboxylic acid, 4,6-bis[4,5-bis(1,3,2-dithiarsolan-2-yl)-3,6-dihydroxy-9H-xanthen-9-yl]- (9CI) (CA INDEX NAME)



RN 223673-82-3 HCA

CN 9H-Xanthene-9-propanamide, N,N'-1,3-propanediylbis[4,5-bis(1,3,2-dithiarsolan-2-yl)-3,6-dihydroxy- (9CI) (CA INDEX NAME)



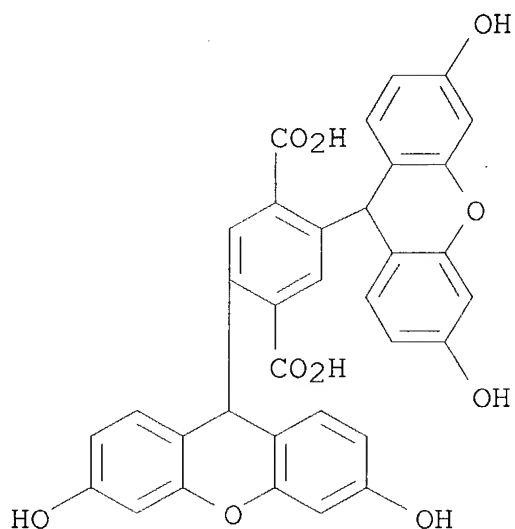
IT 223673-84-5

(target protein sequences for binding of synthetic biarsenical mols.)

RN 223673-84-5 HCA

CN 1,4-Benzenedicarboxylic acid, 2,5-bis(3,6-dihydroxy-9H-xanthen-9-yl)-

(9CI) (CA INDEX NAME)

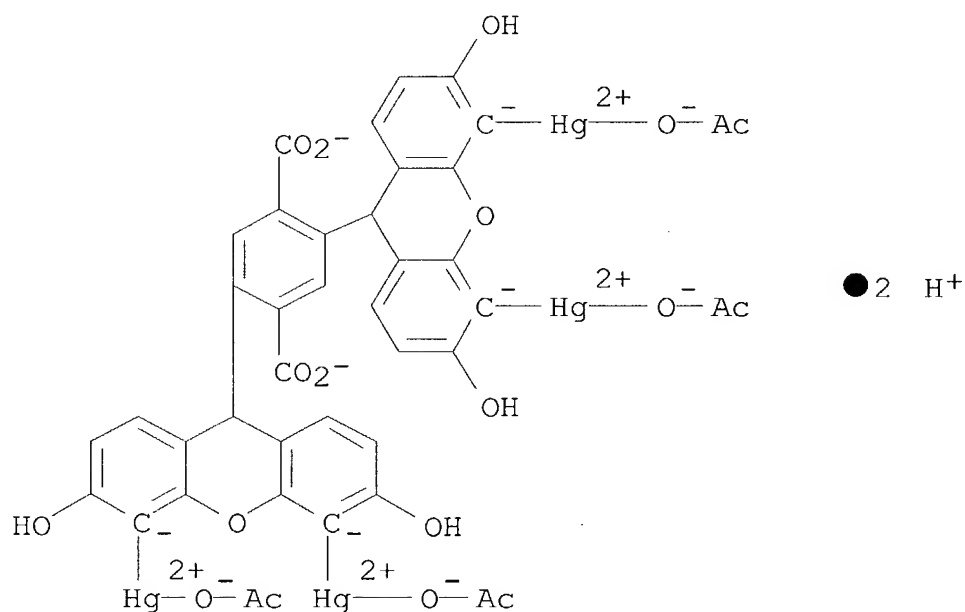


IT 223673-86-7P

(target protein sequences for binding of synthetic biarsenical mols.)

RN 223673-86-7 HCA

CN Mercurate(2-), tetrakis(acetato-.kappa.O)[.mu.-[(2,5-dicarboxylato-1,4-phenylene)bis(3,6-dihydroxy-9H-xanthene-9,4,5-triyl)]]tetra-, dihydrogen (9CI) (CA INDEX NAME)



IC ICM G01N033-566
ICS C07F009-80; C12N015-09; C12N015-64
CC 9-15 (Biochemical Methods)
Section cross-reference(s): 6
IT Peptides, **analysis**
Proteins, specific or class
(labeled; target **protein** sequences for binding of
synthetic biarsenical mols.)
IT Calmodulins
Peptides, **analysis**
Proteins, general, analysis
(target **protein** sequences for binding of synthetic
biarsenical mols.)
IT 52-90-4, L-Cysteine, biological studies
(target protein sequences for binding of synthetic biarsenical
mols.)
IT 223673-80-1 223673-81-2 223673-82-3
(target protein sequences for binding of synthetic biarsenical
mols.)
IT 76-54-0, 2',7'-Dichlorofluorescein 89-05-4, 1,2,4,5-
Benzenetetracarboxylic acid 108-46-3, 1,3-Benzenediol, reactions
540-63-6, 1,2-Ethanedithiol 1600-27-7, Mercuric acetate
7784-34-1, Arsenic trichloride 32382-27-7, Fluorescein mercuric
acetate 223673-84-5
(target protein sequences for binding of synthetic biarsenical
mols.)
IT 54210-30-9P 223673-86-7P 223673-87-8P
(target protein sequences for binding of synthetic biarsenical
mols.)
L98 ANSWER 20 OF 28 HCA COPYRIGHT 2004 ACS on STN
130:264438 Sulfonated xanthene derivatives synthesis and applications as
fluorescent stains. Mao, Fei; Leung, Wai-Yee; Haugland, Richard P.
(Molecular Probes, Inc., USA). PCT Int. Appl. WO 9915517 A1
19990401, 63 pp. DESIGNATED STATES: W: AU, CA, JP, US; RW: AT, BE,
CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE.
(English). CODEN: PIXXD2. APPLICATION: WO 1998-US19921 19980923.
PRIORITY: US 1997-935963 19970923.
AB The present invention describes xanthene dyes, including rhodamines,
rhodols and fluoresceins that are substituted one or more times by a
sulfonic acid or a salt of a sulfonic acid. The dyes of the
invention, including chem. reactive dyes and dye-conjugates are
useful as fluorescent probes, particularly in biol. samples.
IT 9003-53-6DP, Polystyrene, amine deriv.
(fluorescently labeled microspheres; sulfonated xanthene derivs.
synthesis and applications as fluorescent stains)
RN 9003-53-6 HCA
CN Benzene, ethenyl-, homopolymer (9CI) (CA INDEX NAME)

CM 1

CRN 100-42-5

CMF C8 H8

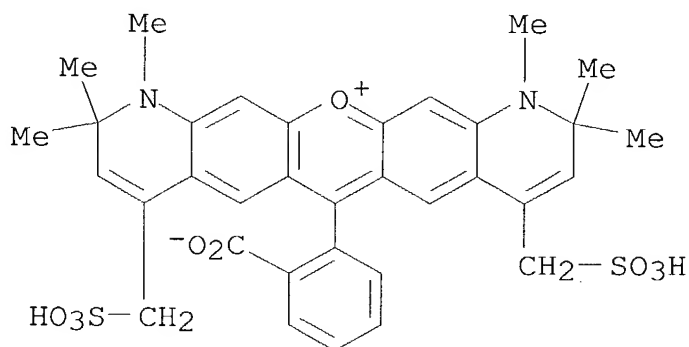
 $\text{H}_2\text{C}=\text{CH}-\text{Ph}$

IT 222165-01-7P 222165-02-8P

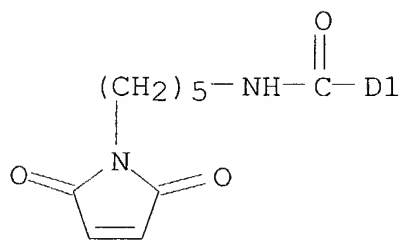
(sulfonated xanthene derivs. synthesis and applications as fluorescent stains)

RN 222165-01-7 HCA

CN Pyrano[3,2-g:5,6-g']diquinol-13-ium, 6-[2-carboxy-4(or 5)-[[[5-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)pentyl]amino]carbonyl]phenyl]-1,2,10,11-tetrahydro-1,2,2,10,10,11-hexamethyl-4,8-bis(sulfomethyl)-, inner salt, monosodium salt (9CI) (CA INDEX NAME)

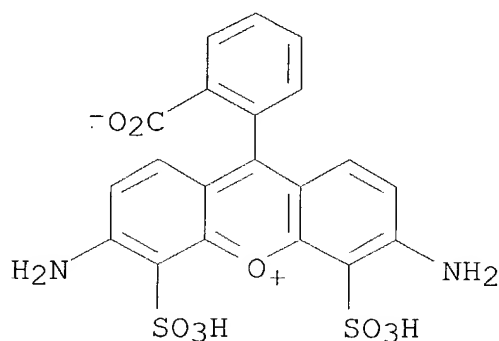


● Na

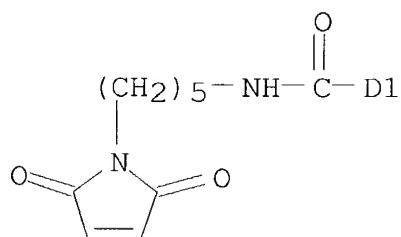


RN 222165-02-8 HCA

CN Xanthylum, 3,6-diamino-9-[2-carboxy-4(or 5)-[[[5-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)pentyl]amino]carbonyl]phenyl]-4,5-disulfo-, inner salt, sodium salt (9CI) (CA INDEX NAME)

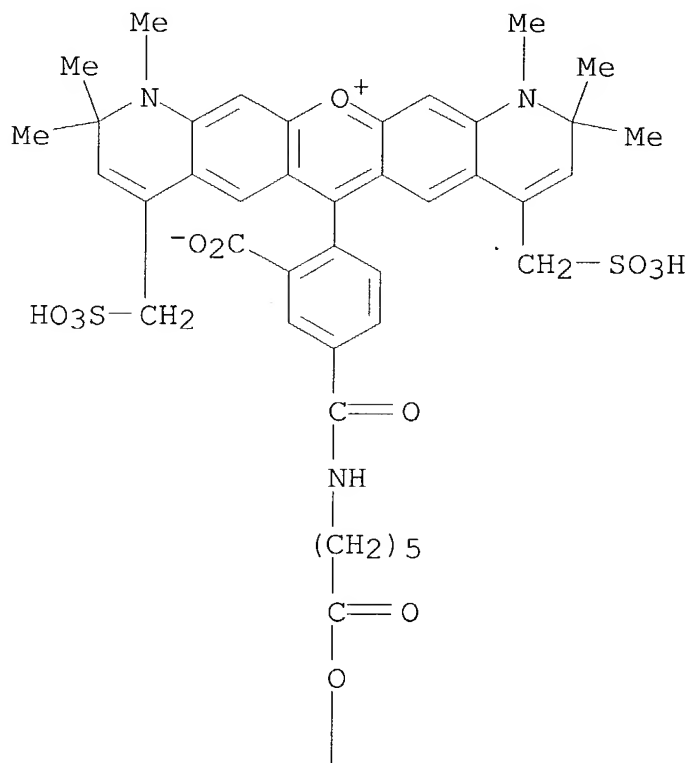


•x Na

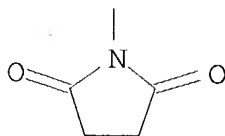


- IT 222159-86-6P 222165-01-7DP, conjugate
(sulfonated xanthene derivs. synthesis and applications as
fluorescent stains)
- RN 222159-86-6 HCA
- CN Pyrano[3,2-g:5,6-g']diquinolin-13-ium, 6-[2-carboxy-4-[[[(2,5-dioxo-
1-pyrrolidinyl)oxy]-6-oxohexyl]amino]carbonyl]phenyl]-1,2,10,11-
tetrahydro-1,2,2,10,10,11-hexamethyl-4,8-bis(sulfomethyl)-, inner
salt, monolithium salt (9CI) (CA INDEX NAME)

PAGE 1-A

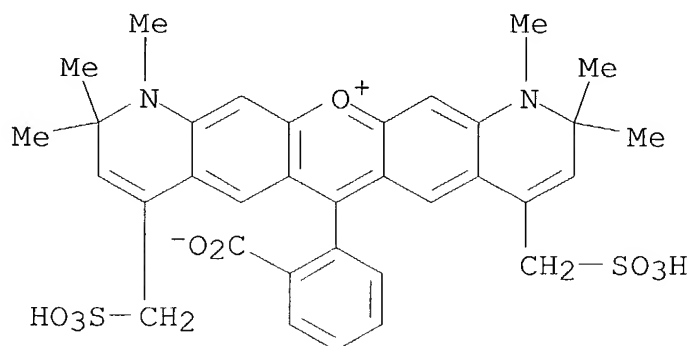


PAGE 2-A

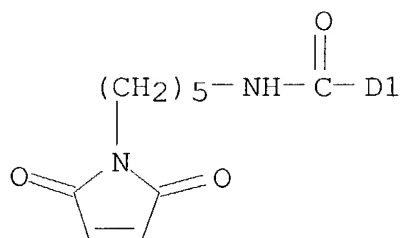


● Li

RN 222165-01-7 HCA
 CN Pyrano[3,2-g:5,6-g']diquinolin-13-ium, 6-[2-carboxy-4(or
 5)-[[[5-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-
 yl)pentyl]amino]carbonyl]phenyl]-1,2,10,11-tetrahydro-1,2,2,10,10,11-
 hexamethyl-4,8-bis(sulfomethyl)-, inner salt, monosodium salt (9CI)
 (CA INDEX NAME)



● Na



- IC ICM C07D311-82
ICS C07D491-14; C07D405-12; C07D491-22; C07H003-06; C07H021-00;
C07H019-04; C07K014-415; G01N001-30
- CC 9-15 (Biochemical Methods)
Section cross-reference(s): 6, 27
- IT **Proteins**, specific or class
(A; sulfonated xanthene derivs. synthesis and applications as
fluorescent stains)
- IT Immunoglobulins
Proteins, specific or class
(G; sulfonated xanthene derivs. synthesis and applications as
fluorescent stains)
- IT Phycoerythrins
(R-phycoerythrins, **pyridyldisulfide** modified;
sulfonated xanthene derivs. synthesis and applications as
fluorescent stains)
- IT **Proteins**, specific or class
(conjugates, sulfonated xanthene conjugate; sulfonated xanthene
derivs. synthesis and applications as fluorescent stains)
- IT Actins
Agglutinins and Lectins
Allophycocyanins
Amino acids, biological studies
Antibodies

Avidins

Biliproteins

Disaccharides

Growth factors, animal

Haptens

Lipids, biological studies

Monosaccharides

Nucleic acids

Nucleotides, biological studies

Peptides, biological studies

Polymers, biological studies

Polysaccharides, biological studies

Toxins

(sulfonated xanthene conjugate; sulfonated xanthene derivs. synthesis and applications as fluorescent stains)

IT **Protein receptors**

(sulfonated xanthene derivs. synthesis and applications as fluorescent stains)

IT **Proteins, general, analysis**

(sulfonated xanthene derivs. synthesis and applications as fluorescent stains)

IT **9003-53-6DP, Polystyrene, amine deriv.**

(fluorescently labeled microspheres; sulfonated xanthene derivs. synthesis and applications as fluorescent stains)

IT 222159-70-8P 222159-72-0P 222159-73-1P 222159-74-2P

222159-79-7P 222159-82-2P 222159-84-4P 222159-85-5P

222164-80-9P 222164-81-0P 222164-92-3P 222164-95-6P

222164-98-9P 222164-99-0P **222165-01-7P**

222165-02-8P 222165-04-0P

(sulfonated xanthene derivs. synthesis and applications as fluorescent stains)

IT 2321-07-5DP, Fluorescein, conjugates 146397-20-8DP, CY-3, conjugates 183185-51-5DP, Rhodol Green, conjugates

189200-71-3DP, Rhodamine Green, conjugates 199745-67-0DP, Texas

Red-X, conjugates 222159-76-4P 222159-78-6P 222159-80-0P

222159-81-1P 222159-82-2DP, conjugate 222159-83-3P

222159-86-6P 222159-92-4DP, conjugate 222159-93-5DP,

conjugate 222164-82-1P 222164-83-2P 222164-86-5DP, conjugate

222164-87-6P 222164-88-7P 222164-91-2P 222164-92-3DP,

conjugate 222164-93-4P 222164-95-6DP, conjugate 222165-00-6P

222165-01-7DP, conjugate 222165-04-0DP, spiperone

conjugate

(sulfonated xanthene derivs. synthesis and applications as fluorescent stains)

L98 ANSWER 21 OF 28 HCA COPYRIGHT 2004 ACS on STN

130:135555 Determination of the **disulfide** bonds within a B

domain variant surface glycoprotein from Trypanosoma congolense.

Bussler, Holm; Linder, Monica; Linder, Dietmar; Reinwald, Erwin (Biochemisches Institut am Klinikum, Justus-Liebig-Universitat, Giessen, 35392, Germany). Journal of Biological Chemistry, 273(49), 32582-32586 (English) 1998. CODEN: JBCHA3. ISSN: 0021-9258. Publisher: American Society for Biochemistry and Molecular Biology.

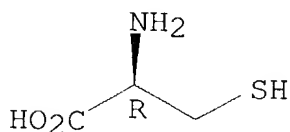
AB The **disulfide** bonds within a variant surface glycoprotein from Trypanosoma congolense have been detd. L-[35S]**Cysteine** metabolically labeled protein was **digested** with trypsin, and **radiolabeled peptides** were sepd. by reversed-phase high performance liq. chromatog., and putative cystine-contg. **peptides** were subdigested with other proteases and analyzed after further purifn. by amino acid sequencing and **mass spectrometry**. All eight **cysteine** residues of the protein, located within the N-terminal domain, are covalently linked. The four **disulfide** bonds are between **cysteines** 16/236, 171/193, 195/206, and 286/298. This is, for the first time, the detn. of **disulfide** bonds within a variant surface glycoprotein belonging to the B-type. As all the eight **cysteines** of BENat 1.3 variant surface glycoprotein are positionally conserved, the cystine pattern of this protein can be regarded as a prototype of **disulfide** bonding within B-type variant surface glycoproteins. Although the **cysteine** residues of B-type variant surface glycoproteins are located at completely different positions in the protein chain compared with A-type variant surface glycoproteins, the positions of the **disulfide** bonds can easily be integrated into the A-type tertiary structure. This result implies that, despite their enormous amino acid sequence variability, variant surface glycoproteins, regardless of their subtype, can fold into a similar tertiary structure.

IT 52-90-4, L-**Cysteine**, biological studies
(detn. of **disulfide** bonds within a B domain variant surface glycoprotein from Trypanosoma congolense)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



CC 6-3 (General Biochemistry)

Section cross-reference(s): 10

ST variant surface glycoprotein BENat13 **disulfide** bond

- location Trypanosoma
- IT Glycolipoproteins
(VSG, BENat 1.3; detn. of **disulfide** bonds within a B domain variant surface glycoprotein from Trypanosoma congolense)
- IT **Disulfide** group
Trypanosoma congolense
(detn. of **disulfide** bonds within a B domain variant surface glycoprotein from Trypanosoma congolense)
- IT Tertiary structure
(**protein**; detn. of **disulfide** bonds within a B domain variant surface glycoprotein from Trypanosoma congolense)
- IT 52-90-4, L-Cysteine, biological studies
(detn. of **disulfide** bonds within a B domain variant surface glycoprotein from Trypanosoma congolense)

L98 ANSWER 22 OF 28 HCA COPYRIGHT 2004 ACS on STN

123:50239 Production and Properties of Skeletal Myosin Subfragment 1 Selectively Labeled with Fluorescein at Lysine-553 Proximal to the Strong Actin-Binding Site. Bertrand, Raoul; Derancourt, Jean; Kassab, Rhida (Centre de Recherches de Biochimie Macromoléculaire, Université de Montpellier I, Montpellier, 34033, Fr.). Biochemistry, 34(29), 9500-7 (English) 1995. CODEN: BICHAW. ISSN: 0006-2960. Publisher: American Chemical Society.

- AB We describe, for the first time, the reaction of skeletal myosin subfragment 1 (S-1) with the succinimido ester of 6-[fluorescein-5(and 6)-carboxamido]hexanoic acid (FHS), which takes place at pH 7.0, 20 .degree.C, within a 15 min period, in the presence of 1.5-1.8-fold molar excess of reagent over **protein**. As a result, 0.9-1.0 mol of fluorescyl group/mol of S-1 was covalently incorporated exclusively into the 95 kDa heavy chain as monitored by spectroscopic measurements. The central 50 kDa segment included the main site of fluorescence attachment as assessed by gel electrophoresis. The extent of S-1-FHS conjugation is strongly sensitive to F-actin binding but not to the interaction of nucleotides. The formation of the rigor F-actin-S-1 complex decreased the level of S-1 labeling to 20% without any competition between actin and S-1 for FHS binding. The derivatization of S-1 did not alter the K+-ATPase activity, but it enhanced the Ca2+-ATPase and Mg2+-ATPase to 150% and 225%, resp., whereas it lowered the actin-activated ATPase to only 75% of the original activity. A double-reciprocal plot of the ATPase rate against actin concn. indicated a 2-fold decrease of the Vmax value for modified S-1, while the Km for actin was unchanged. Cosedimentation expts. did not reveal disruption of the rigor acto-S-1 interaction by the bound fluorophore. The labeled S-1 heavy chain was isolated, and its total tryptic **digest** was fractionated by reverse-phase HPLC. Only two fluorescent peptides, designated P-1 and P-2, contg.

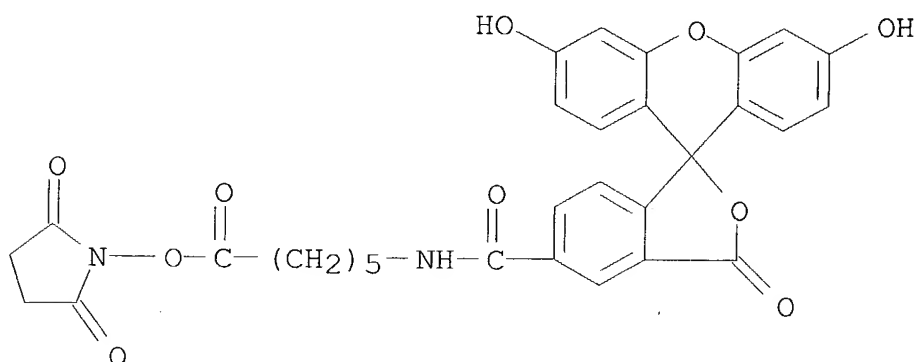
15% and 85%, resp., of the initial fluorescence were found, and after purifn. they were entirely sequenced. The major P-2 peptide spanned the heavy chain sequence Ala-545-Lys-561 with Lys-553 identified as the FHS-hyperreactive residue; the sequence of the minor P-1 peptide corresponded to Gly-638-Lys-641 with Lys-640 being linked to FHS. The location of Lys-553 in the S-1 primary structure is of particular interest as it is relevant to the primary stereospecific and hydrophobic actin-binding site thought to involve the helix(Gly-516-Phe-542)-loop(Pro-543-Thr-546)-helix(Asp-547-His-558) motif residing in the lower subdomain of the 50 kDa region. Lys-553 is positioned at the end of the latter helix, and the fluorescyl group bound to it may represent a valuable landmark to probe the functioning and orientational properties of this strategic S-1 area during the acto-S-1-ATP interactions.

IT 148356-00-7 148356-01-8

(myosin subfragment 1 selectively labeled with fluorescein at lysine-553 proximal to the actin-binding site)

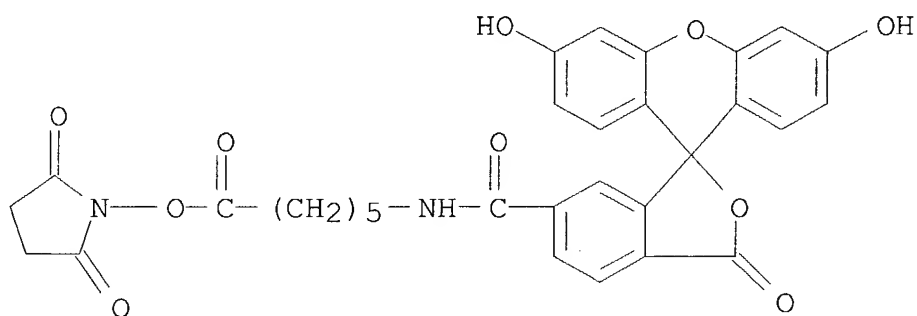
RN 148356-00-7 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-5-carboxamide,
N-[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)



RN 148356-01-8 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-6-carboxamide,
N-[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)



CC 6-3 (General Biochemistry)

IT 148356-00-7 148356-01-8

(myosin subfragment 1 selectively labeled with fluorescein at lysine-553 proximal to the actin-binding site)

L98 ANSWER 23 OF 28 HCA COPYRIGHT 2004 ACS on STN

122:234841 Specific binding assay compound with inhibitive self-quenching characteristics. Kline, Stanley (Enzo Diagnostics, Inc., USA). U.S. US 5384241 A 19950124, 6 pp. Cont. of U.S. Ser. No. 96,182, abandoned. (English). CODEN: USXXAM. APPLICATION: US 1989-443812 19891129. PRIORITY: US 1987-96182 19870911.

AB Disclosed is an assay system including a compd. comprising an analyte-specific moiety having substituted thereon a polymer comprising plurality of self-quenching emitter moieties and a plurality of isocharged functionality sepg. the emitter moieties. The present invention provides compds. that overcome the undesirable effects of self-quenching when multiple emitter moieties are used for labeling of assay reagents. Avoidance of this self-quenching phenomenon by the compds. of the invention makes it possible to introduce a more concd. degree of labeling onto analyte-specific mols. such as oligonucleotide probes, antibodies and other specific binding **proteins** and analyte-specific polysaccharides. Therefore, it is possible to effect greater assay sensitivity because the no. of labels per recognition mol. (analyte-specific moiety) can be increased beyond the point previously possible without the redn. in signal caused by self-quenching.

IT 162224-11-5P

(specific binding assay compd. with inhibitive self-quenching characteristics)

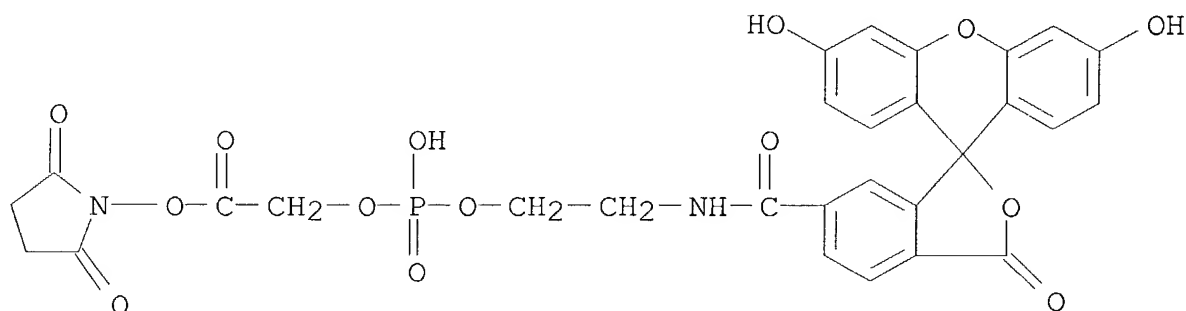
RN 162224-11-5 HCA

CN Phosphoric acid, mono[2-[[[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-6-yl)carbonyl]amino]ethyl] mono[2-[(2,5-dioxo-1-pyrrolidinyl)oxy]-2-oxoethyl] ester, polymer with aziridine (9CI) (CA INDEX NAME)

CM 1

CRN 162224-04-6

CMF C29 H23 N2 O14 P



CM 2

CRN 151-56-4

CMF C2 H5 N

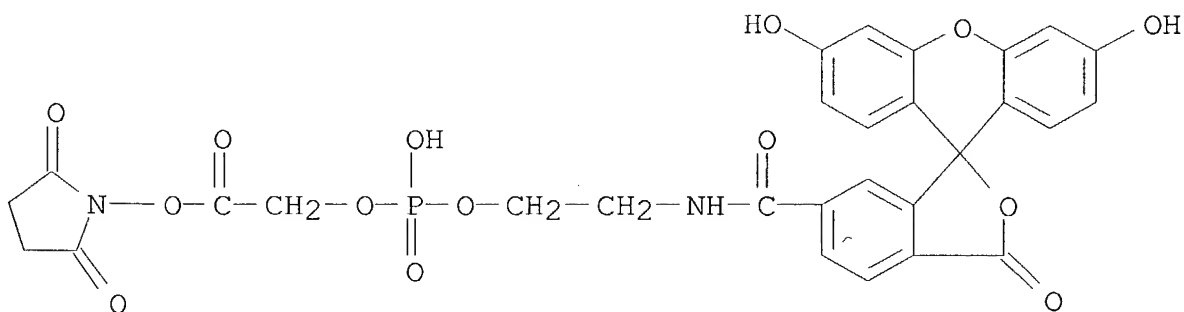


IT 162224-04-6P

(specific binding assay compd. with inhibitive self-quenching characteristics)

RN 162224-04-6 HCA

CN Phosphoric acid, mono[2-[[[3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-6-yl)carbonyl]amino]ethyl] mono[2-[(2,5-dioxo-1-pyrrolidinyl)oxy]-2-oxoethyl] ester (9CI) (CA INDEX NAME)

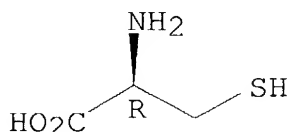


- IC ICM C07H021-00
ICS G01N033-53; C12Q001-68
NCL 435006000
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 3, 15
IT Dyes
Fluorescence quenching
Fluorescent substances
Isotope indicators
Nucleic acid hybridization
Phosphorescent substances
(specific binding assay compd. with inhibitive self-quenching characteristics)
IT **Proteins**, uses
(specific binding assay compd. with inhibitive self-quenching characteristics)
IT 9002-98-6DP, reaction with fluorescein derivs. 92557-81-8DP,
conjugates with polymers and biopolymers 162224-03-5P
162224-11-5P 162224-12-6P
(specific binding assay compd. with inhibitive self-quenching characteristics)
IT **162224-04-6P**
(specific binding assay compd. with inhibitive self-quenching characteristics)
- L98 ANSWER 24 OF 28 HCA COPYRIGHT 2004 ACS on STN
120:107724 Influence of the spectroscopic potential energy function
SPASIBA on molecular dynamics of proteins: comparison with the AMBER
potential. Derreumaux, Philippe; Vergoten, Gerard (INSERM U279 (SDI
15721), rue du Professeur Calmette, Lille, 59000, Fr.). THEOCHEM,
105(1-3), 55-64 (English) 1993. CODEN: THEODJ. ISSN: 0166-1280.
AB The SPASIBA potential energy function developed for proteins on the
basis of vibrational frequencies of **peptides** is compared
to the AMBER force field by studying the mol. conformational
flexibility of the alanine .alpha.-decapeptide and Ecballium
elaterium trypsin inhibitor II (EETI-II), a 28-residues
peptide. Two mol. dynamics (MD) simulations of 500ps
duration using a distance-dependent dielec. function were carried
out for the decapeptide with two different bond angle potential
representations: the classical harmonic bond angle potential and the
combination of this potential and the 1-3 geminal Urey-Bradley
potential. The authors also performed two 200ps simulations of
EETI-II with a sigmoidal distance-dependent function and examd. the
effects of the V1-4tg energetics component, which deals with the 1-4
vicinal interactions taking effect on the dynamics in some
side-chains. In comparing the MD results, the two potentials that
better reproduce the obsd. vibrational frequencies act differently

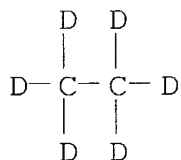
on the flexibility of proteins. On the one hand, the Urey-Bradley potential increases the mobilities of backbone atoms; on the other hand, the V1-4tg potential generally constraints the side-chains to explore fewer conformations. Together, these results are in agreement with a better fit of the x-ray temp. factors, but do not give a new dynamic picture of proteins on a time scale less than 1ns, because localized rather than collective conformational changes are generated.

IT 52-90-4, Cysteine, properties 1632-99-1,
Hexadeuteroethane 1735-17-7, Cyclohexane-d12
(effect of potential energy functions on mol. dynamics calcns.)
RN 52-90-4 HCA
CN L-Cysteine (9CI) (CA INDEX NAME)

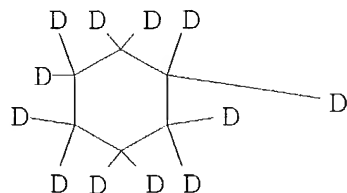
Absolute stereochemistry.



RN 1632-99-1 HCA
CN Ethane-d6 (6CI, 8CI, 9CI) (CA INDEX NAME)



RN 1735-17-7 HCA
CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



CC 34-3 (Amino Acids, Peptides, and Proteins)
Section cross-reference(s): 22
ST mol dynamics **calcn peptide protein**;
spectroscopic energy function mol dynamics
IT **Peptides**, properties

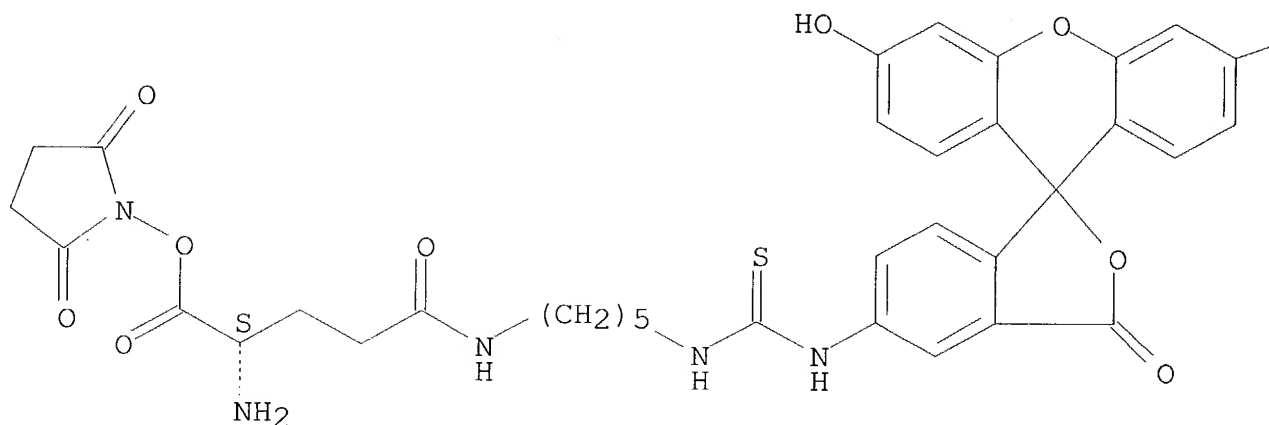
- Proteins, properties
(effect of potential energy functions on conformations from mol. dynamics calcns.)
- IT Simulation and Modeling, physicochemical
(mol. dynamics, effect of potential energy functions on **peptide** and protein conformations from mol. dynamics calcns.)
- IT **52-90-4, Cysteine**, properties 61-90-5, Leucine, properties 64-17-5, Ethanol, properties 72-19-5, Threonine, properties 74-82-8, Methane, properties 74-84-0, Ethane, properties 74-98-6, Propane, properties 75-08-1, Ethanethiol 75-28-5, Isobutane 78-78-4, 2-Methylbutane 79-05-0, Propionamide 79-16-3, N-Methylacetamide 110-82-7, Cyclohexane, properties 111-65-9, Octane, properties 124-18-5, Decane 463-82-1, Neopentane 624-89-5, Ethyl methyl sulfide 624-92-0, Dimethyl **disulfide** 1118-69-0, N-Isopropylacetamide **1632-99-1**, Hexadeuteroethane **1735-17-7**, Cyclohexane-d12 2675-88-9, N-Methylisobutyramide 7154-79-2, 2,2,3,3-Tetramethylpentane 13054-03-0, Glycyl-L-prolylglycylglycine
(effect of potential energy functions on mol. dynamics calcns.)
- L98 ANSWER 25 OF 28 HCA COPYRIGHT 2004 ACS on STN
- 114:203058 Affinity labeling of folate transport **proteins** with the N-hydroxysuccinimide ester of .gamma.-isomer of fluorescein-methotrexate. Fan, Jianguo; Pope, Laura E.; Vitols, Karin S.; Huennekens, F. M. (Res. Inst., Scripps Clin., La Jolla, CA, 92037, USA). Biochemistry, 30(18), 4573-80 (English) 1991. CODEN: BICHAW. ISSN: 0006-2960.
- AB Fluorescein-methotrexate, a deriv. in which the fluorophore is linked via a diaminopentane spacer to either the .alpha.- and .gamma.-carboxyl group of the glutamate moiety in the drug (Gapski et al., 1975), has been synthesized by an improved procedure and sepd. by DEAE-Trisacryl chromatog. into the .alpha.- and .gamma.-isomers (.alpha.-F-MTX and .gamma.-F-MTX). Each isomer was characterized by **mass spectrometry**, elemental anal., absorbance spectrum, TLC, and reversed-phase HPLC. Identity of the isomers was established by the following enzymic criteria: (a) .gamma.-F-MTX (but not the .alpha.-isomer) was hydrolyzed at the pterate-glutamate bond by carboxypeptidase G2 to yield 4-amino-4-deoxy-10-methylpterate and .gamma.-glutamyl-diaminopentane-fluorescein; and (b) .gamma.-F-MTX was a much better inhibitor of human dihydrofolate reductase than the .alpha.-isomer (Ki values of 0.079 and 4.6 nM). .alpha.- And .gamma.-F-MTX were comparable as inhibitors (Ki values of 1.6 and 0.6 .mu.M) of the transport system for reduced folates and MTX in L1210 cells, but the transporter in Lactobacillus casei was inhibited only by the .gamma.-isomer (Ki = 4.3 .mu.M). The .gamma.-isomer, therefore, was selected for

covalent labeling of **proteins**. When L. casei folate transport **protein** (18 kDa) was treated with .gamma.-F-MTX that had been activated with N-hydroxysuccinimide (NHS), the **protein** was readily visualized as a fluorescent band on SDS-PAGE electrophoretograms. The probe was also able to detect the transporter in membranes. SDS-PAGE anal. of a Triton X 100 ext. of L. casei membrane fragments that had been pretreated with activated .gamma.-F-MTX revealed only 2 fluorescent-labeled bands, viz., the 18-kDa transporter and an unidentified 33-kDa **protein**. The 43-kDa transporter for reduced folate compds. and MTX in L1210 cells was also labeled by this procedure but, because of its relatively low level, visualization required immunopurifn., SDS-PAGE, and transfer to nitrocellulose, followed by immunoblotting with rabbit anti-fluorescein antibody/biotinylated goat anti-rabbit IgG/streptavidin-peroxidase conjugate. NHS-activated .gamma.-F-MTX also facilitated visualization, via fluorescence microscopy, of folate transporters on individual L1210 cells. The validity of this procedure was demonstrated by the marked redn. in fluorescence when labeling was conducted in the presence of excess MTX or when a mutant subline (R81) down-regulated for the transporter was used. L. casei spheroplasts treated with NHS-activated .gamma.-F-MTX were also fluorescent, and specificity was shown by reduced labeling in the presence of MTX. In this instance, however, the 33-kDa **protein** rather than the transporter appeared to be the labeled component.

IT 132884-74-3P
(prepn. of, for folate-transportin **protein** affinity labeling)
RN 132884-74-3 HCA
CN Pentanamide, 4-amino-N-[5-[[[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)amino]thioxomethyl]amino]pentyl]-5-[(2,5-dioxo-1-pyrrolidinyl)oxy]-5-oxo-, (S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

—OH

- CC 9-15 (Biochemical Methods)
Section cross-reference(s): 6
- ST folate transport **protein** affinity labeling; fluorescein
methotrexate ester **protein** affinity labeling
- IT Lactobacillus casei
(folate-transporting **proteins** affinity labeling in, by
fluorescein methotrexate hydroxysuccinimidyl ester)
- IT Affinity
(labeling by, of folate-transporting **proteins**)
- IT Microscopy
(fluorescence, of folate-transport **proteins**,
fluorescein methotrexate hydroxysuccinimidyl ester in)
- IT **Proteins**, specific or class
(folate-transporting, affinity labeling of, with fluorescein
methotrexate hydroxysuccinimidyl ester)
- IT 132884-72-1P
(prepn. of, folate-transporting **protein** affinity
labeling in relation to)
- IT 132884-74-3P
(prepn. of, for folate-transportin **protein** affinity
labeling)
- L98 ANSWER 26 OF 28 HCA COPYRIGHT 2004 ACS on STN
111:228613 Fluorescein-conjugated **proteins** with enhanced
fluorescence. Ronald, Robert C.; Nguyen Phuc Huu; Rowley, Gerald L.

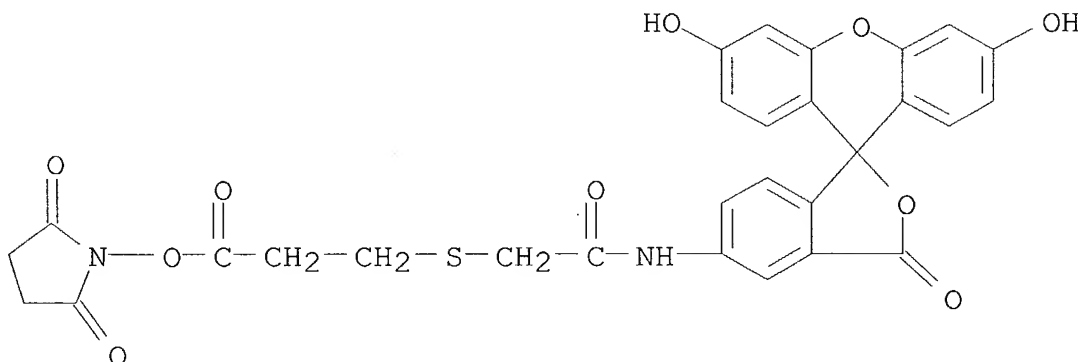
(Sclavo, Inc., USA). PCT Int. Appl. WO 8900291 A1 19890112, 30 pp. DESIGNATED STATES: W: AU, JP; RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1988-US2240 19880701. PRIORITY: US 1987-69288 19870701.

AB A method for detn. of an analyte, which comprises at least the step of binding a fluorescent-labeled reagent to the analyte, uses a fluorescent-labeled reagent which is a ligand labeled with a substituent FlNHCZCR2 (I; Fl = fluorescein; Z = O, S; R = H, C1-4 alkyl). Fluorescein I (5-Fl-NHCOCH2S(CH2)2COOEt) (II) was prepd. from the reaction of 3-mercaptopropionic acid (80 .mu.L in 6 mL DMF and 3 mL 50 mM phosphate, 2.5 mM EDTA buffer, pH 6.30) with 5-iodoacetamidofluorescein (200 mg in 7 mL DMF and 4 mL of the same buffer) in Tris buffer overnight at 50.degree.. II 1.28 was reacted with N-hydroxysuccinimide 3.45 and 1-(3-dimethylaminopropyl)-3-ethylcarbodiimide 4.22 mg in anhyd. DMF for 7 h at room temp. The resultant N-hydroxysuccinimide ester was conjugated to rabbit IgG Fab' fragments, which were then conjugated to .alpha.-**fetoprotein** through a sulfosuccinimidyl linker. Patient serum samples, the labeled .alpha.-**fetoprotein** reagent, buffer, and goat anti-.alpha.-**fetoprotein** antibody were mixed and incubated for 2.5 h at 37.degree.. Rabbit antigoat Ig antibody was added, followed by PEG and incubation for 30 min at room temp. The ppt. was dissolved in measurement buffer and fluorescence was measured. .alpha.-**Fetoprotein** was detd. by comparison to a std. curve.

IT 123761-26-2P 123761-28-4P
(prepn. of, as fluorescent label)

RN 123761-26-2 HCA

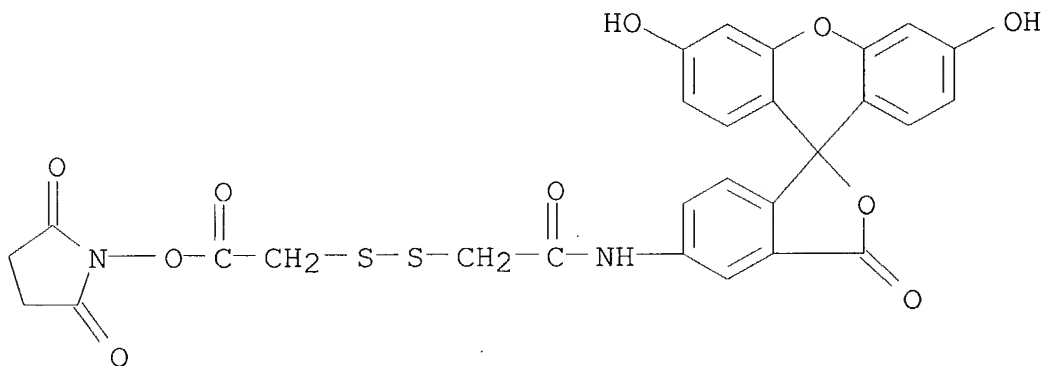
CN Acetamide, N-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)-2-[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]- (9CI) (CA INDEX NAME)



RN 123761-28-4 HCA

CN Acetamide, N-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)-2-[[2-[(2,5-dioxo-1-pyrrolidinyl)oxy]-2-

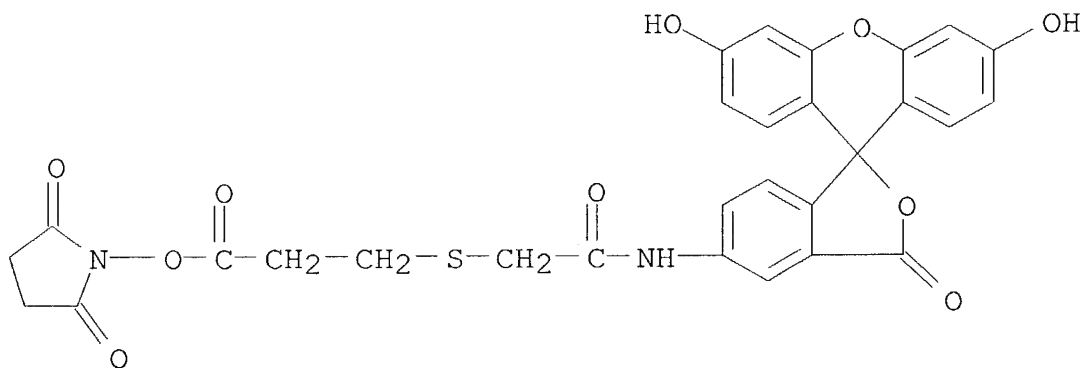
oxoethyl]dithio]- (9CI) (CA INDEX NAME)



IT 123761-26-2DP, IgG reaction products, .alpha.-
fetoprotein conjugates
(prepn. of, as fluorescent tracer)

RN 123761-26-2 HCA

CN Acetamide, N-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-
[9H]xanthen]-5-yl)-2-[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-
oxopropyl]thio]- (9CI) (CA INDEX NAME)



IC ICM G01N033-53

ICS G01N033-533; C07D311-82

CC 9-14 (Biochemical Methods)

Section cross-reference(s): 28, 79, 80

ST fluorescein amido deriv **protein** label; **fetoprotein**
fluorescein label immunoassay

IT Ligands

Proteins, uses and miscellaneous

(fluorescein-labeled, for fluorescence anal.)

IT Blood analysis

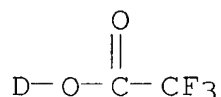
(.alpha.-**fetoprotein** immunochem. detn. in human,
fluorescein deriv.-labeled .alpha.-**fetoprotein** in)

- IT Immunoglobulins
(G, reaction products, with acetamidofluorescein succinimide ester, .alpha.-**fetoprotein** conjugates, prepn. of, as fluorescent tracer)
- IT **Fetoproteins**
(.alpha.-, conjugates, with fluorescein deriv.-labeled IgG Fab', prepn. of, for .alpha.-**fetoprotein** immunochem. detn. in serum)
- IT 120858-32-4P 123740-08-9P **123761-26-2P** 123761-27-3P
123761-28-4P
(prepn. of, as fluorescent label)
- IT **123761-26-2DP**, IgG reaction products, .alpha.-**fetoprotein** conjugates
(prepn. of, as fluorescent tracer)
- IT 103708-09-4DP, .alpha.-**fetoprotein** reaction products
(prepn. of, in prepn. of fluorescent tracer)
- L98 ANSWER 27 OF 28 HCA COPYRIGHT 2004 ACS on STN
- 109:69743 Rapid **analysis** of **proteins** and peptides by reversed-phase chromatography and polymeric micropellicular sorbents. Maa, Yih Fen; Horvath, Csaba (Dep. Chem. Eng., Yale Univ., New Haven, CT, 06520, USA). Journal of Chromatography, 445(1), 71-86 (English) 1988. CODEN: JOCRAM. ISSN: 0021-9673.
- AB Peptides and proteins were sepd. by reversed-phase chromatog. on a 30 .times. 4.6 mm I.D. column packed with nonporous crosslinked **polystyrene** particles having a mean particle diam. of 3 .mu.m and a rugulose surface. The polymeric support did swell slightly in org. solvents, but the estd. 5-8% change in particle diam. did not adversely affect the efficiency of the column which was used repeatedly with gradient elution from water to org. solvent under conditions typically employed in reversed-phase chromatog. In these expts., the pH of the eluent was varied in a wide range to compare the effect of acidic and alk. eluents on the sepn. of protein and complex peptide mixts. The column showed no deterioration even after extensive exposure to alk. mobile phases. The retention behavior of 16 proteins having widely different pI values was studied as a function of the eluent pH. The chromatog. system exhibited large selectivity differences upon changing the pH of the eluent from 2 to 11. Anal. information about peptide and protein mixts. could therefore be enhanced by using eluents at the pH extremes. At the pH extremes of 2 and 11 peak sharpness and protein mass recovery were superior to those obtained with neutral eluents. Usually the column temp. was held at 80.degree. and typical anal. times ranged from 30 s to 10 min as illustrated by chromatograms of protein mixts. and by peptide maps. With regular use under such conditions, the column showed no deterioration after 3 mo.
- IT 599-00-8

(in proteins reversed-phase HPLC)

RN 599-00-8 HCA

CN Acetic acid-d, trifluoro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



CC 9-3 (Biochemical Methods)

IT Agglutinins and Lectins

Albumins, analysis

Conalbumins

Fetuin

Hemoglobins

Myoglobins

Ovalbumins

Peptides, analysis

Proteins, analysis

Transferrins

(chromatog. of, reversed-phase high-performance liq., on polymeric micropellicular sorbent)

IT 9003-70-7, **Styrene**-divinylbenzene copolymer

(as stationary phase, in reversed-phase HPLC of peptides and protein)

IT 599-00-8

(in proteins reversed-phase HPLC)

L98 ANSWER 28 OF 28 HCA COPYRIGHT 2004 ACS on STN

107:52516 Isolation of products and intermediates of pancreatic prosomatostatin processing: use of fast atom bombardment **mass spectrometry** as an aid in analysis of prohormone processing. Andrews, P. C.; Dixon, Jack E. (Dep. Biochem., Purdue Univ., West Lafayette, IN, 47907, USA). Biochemistry, 26(15), 4853-61 (English) 1987. CODEN: BICHAW. ISSN: 0006-2960.

AB Major products and an intermediate in the proteolytic processing pathway of preprosomatostatin I from anglerfish (*Lophius americanus*) were purified and characterized. Proteolytic mapping by fast atom bombardment **mass spectrometry** was used to rapidly locate regions of the **peptides** whose masses deviated from those deduced from the cDNA sequence. Amino acid anal. and partial Edman sequencing were also used to confirm the structure. The **protein** structural data **indicate** a glutamate for glycine substitution at position 83 of preprosomatostatin I (aPPSS-I, numbering from the initiator methionine) relative to the cDNA sequence. Two of the **peptides** isolated, aPPSS-I (26-52) (7.5 nmol/g), and aPPSS-I

(26-92) (49.5 nmol/g), define signal cleavage as occurring between **cysteine** and serine at positions 25 and 26, resp. A partial sequence was obtained from fragment ions in the **mass spectrum** of a **peptide** corresponding to aPPSS-I (94-105) (58 nmol/g). The 14-residue somatostatin [**SS-14** corresponding to aPPSS-I (108-121)] was isolated previously. Taken together, these **peptides** suggest a pathway for prosomatostatin I processing in which the residues corresponding to **SS-14** and the immediately preceding 14 residues are cleaved from the prohormone via endoproteolysis (order of cleavage not detd.). The fragment aPPSS-I (94-105) was isolated in lower yield than **SS-14** and may represent a secondary site of cleavage. Subsequent cleavage at arginine-53 results in the minor **peptide** aPPSS-I (26-52). The terminal basic amino acids generated by endoproteolytic processing were not found for any of the **peptides** isolated. The **peptides** described were identified as products of aPPSS-I processing in **radiolabeling** studies with intact anglerfish islets.

CC 2-6 (Mammalian Hormones)
Section cross-reference(s): 12

=> d 199 1-28 cbib abs hitstr hitind

L99 ANSWER 1 OF 28 HCA COPYRIGHT 2004 ACS on STN
139:113655 Fluorescent serine protease affinity labeling agents and methods for determining apoptotic state of cells. Phelps, David J.; Johnson, Gary L.; Lee, Brian W.; Darzynkiewicz, Zbigniew; Grabarek, Jerzy (Immunochemistry Technologies, LLC, USA). PCT Int. Appl. WO 2003059877 A2 20030724, 53 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-US40920 20021219. PRIORITY: US 2001-PV342955 20011221.

AB The invention provides novel serine protease affinity labels L-A-X-NHCH(R')C(:O)CH₂Cl (L = label; A = bond or linker; X = absent, amino acid, **peptide**; R' = H, (substituted)C1-6-alkyl) or salts thereof, as well as compns. comprising such compds. or salts. The compn. of the amino acid side-chain (R') along with the amino acid or amino acid sequence (**peptide**) of the X component of the affinity label affect the target selectivity of the labeled affinity ligand. Utilization of cell-permeable, enzyme-selective,

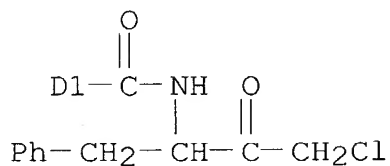
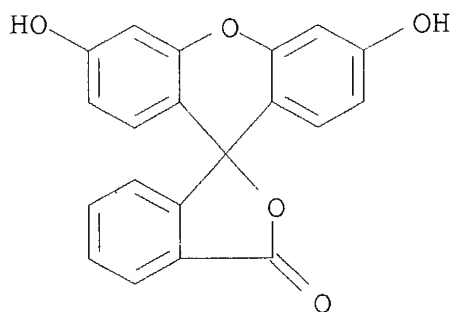
labeled affinity ligands provides a precise mechanism for evaluating the current and future status of cell populations. Thus, the induction of **proteinases** in camptothecin-treated HL-60 cells was obsd. by fluorescence microscopy after addn. of serine **proteinase** affinity inhibitors 5(6)-carboxyfluoresceinyl-L-phenylalanylchloromethyl ketone (FFCK) and 5(6)-carboxyfluoresceinyl-L-leucylchloromethyl ketone (FLCK) and caspase affinity inhibitor 5(6)-carboxyfluoresceinyl-L-valylalanylaspartylfluoromethyl ketone (FAM-VAD-FMK).

IT 474255-88-4

(FFCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

RN 474255-88-4 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-ar-carboxamide,
N-[(1S)-3-chloro-2-oxo-1-(phenylmethyl)propyl]-3',6'-dihydroxy-
(9CI) (CA INDEX NAME)

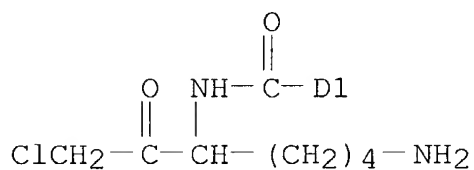
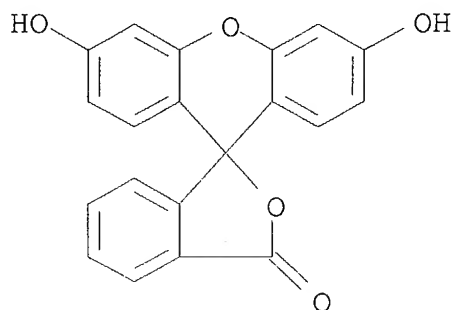


IT 560094-67-9

(FKCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

RN 560094-67-9 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-ar-carboxamide,
N-[(1S)-5-amino-1-(chloroacetyl)pentyl]-3',6'-dihydroxy-3-oxo- (9CI)
(CA INDEX NAME)

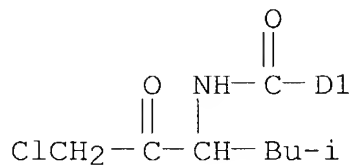
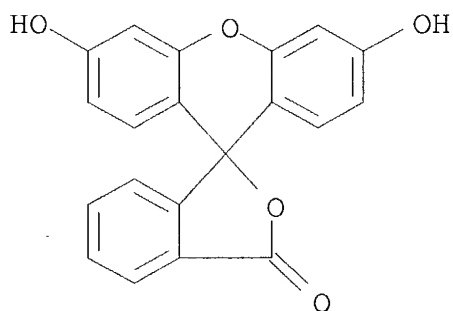


IT 475570-57-1

(FLCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

RN 475570-57-1 HCA

CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-ar-carboxamide,
 N-[(1S)-1-(chloroacetyl)-3-methylbutyl]-3',6'-dihydroxy-3-oxo- (9CI)
 (CA INDEX NAME)

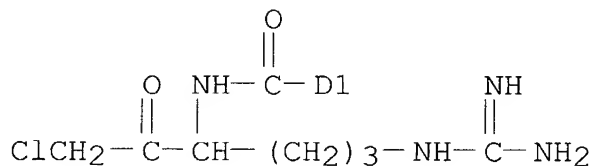
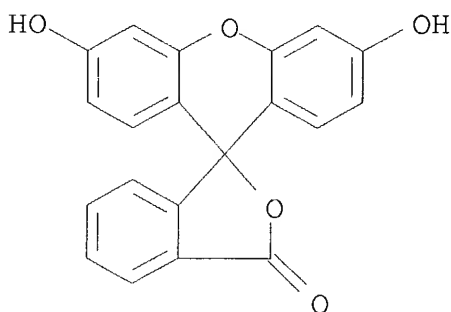


IT 560094-68-0

(FRCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

RN 560094-68-0 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-ar-carboxamide,
N-[(1S)-4-[(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]-3',6'-
dihydroxy-3-oxo- (9CI) (CA INDEX NAME)



IC ICM C07D

CC 7-1 (Enzymes)

Section cross-reference(s): 1

ST apoptosis serine **proteinase** fluorescent affinity label;
disease cancer **diagnosis** serine **proteinase**
fluorescent affinity label

IT 474255-88-4

(FFCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

IT 560094-67-9

(FKCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

IT 475570-57-1

(FLCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

IT 560094-68-0

(FRCK; fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

IT 37259-58-8, Serine **proteinase** 186322-81-6, Caspase

(fluorescent serine protease affinity labeling agents and methods for detg. apoptotic state of cells)

L99 ANSWER 2 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:397832 NMR Structure of a Bifunctional Rhodamine Labeled N-Domain of Troponin C Complexed with the Regulatory "Switch" **Peptide** from Troponin I: Implications for in Situ Fluorescence Studies in Muscle Fibers. Mercier, Pascal; Ferguson, Roisean E.; Irving, Malcolm; Corrie, John E. T.; Trentham, David R.; Sykes, Brian D. (CIHR Group in Protein Structure and Function, Department of Biochemistry, University of Alberta, Edmonton, AB, T6G 2H7, Can.). Biochemistry, 42(15), 4333-4348 (English) 2003. CODEN: BICHAW. ISSN: 0006-2960. Publisher: American Chemical Society.

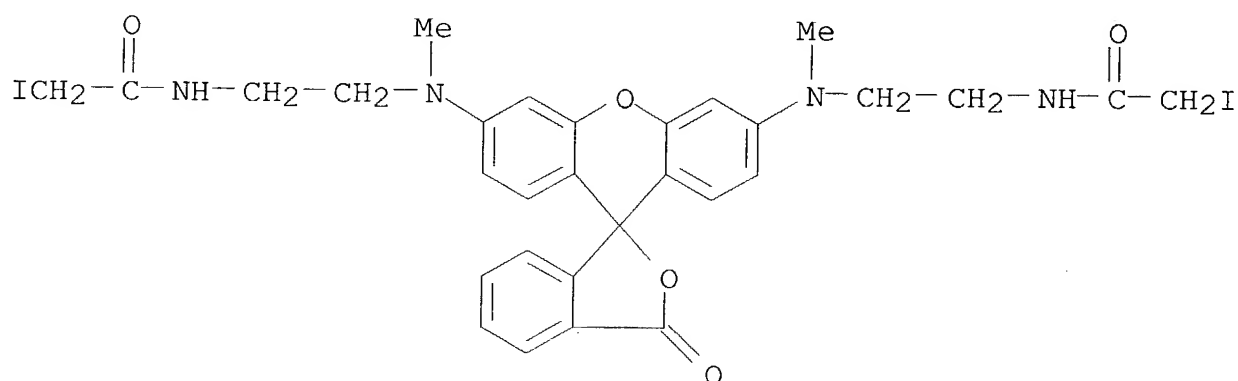
AB The structure of the calcium-satd. regulatory domain of skeletal troponin C (sNTnC) complexed with the switch **peptide** comprising residues 115-131 of troponin I (TnI), and with a bifunctional rhodamine fluorescent label attached to residues 56 (E56C) and 63 (E63C) on the C helix of sNTnC, has been detd. using NMR spectroscopy. The structure shows that the integrity of the C helix is not altered by the E(56,63)C mutations or by the presence of the bifunctional rhodamine and that the label does not interact with the hydrophobic cleft of sNTnC. Moreover, the overall fold of the **protein** and the position of the TnI **peptide** are similar to those obsd. previously with related cardiac NTnC complexes with residues 147-163 of cardiac TnI [Li et al. (1999) Biochem. 38, 8289-8298] and including the drug bepridil [Wang et al. (2002) J. Biol. Chem. 277, 31124-31133]. The degree of opening of the structure is reduced as compared to that of calcium-satd. sNTnC in the absence of the switch **peptide** [Gagne et al. (1995) Nat. Struct. Biol. 2, 784-789]. The switch **peptide** is bound in a shallow and complementary hydrophobic surface cleft largely defined by helices A and B and also has key ionic interactions with sNTnC. These results show that bifunctional rhodamine probes can be attached to surface helices via suitable pairs of solvent-accessible residues that have been mutated to **cysteines**, without altering the conformation of the labeled domain. A set of such probes can be used to det. the orientation and motion of the target domain in the cellular environment [Corrie et al. (1999) Nature 400, 425-430; Ferguson et al. (2003) Mol. Cell 11(4), in press].

IT 203580-70-5

(bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)

RN 203580-70-5 HCA

CN Acetamide, N,N'-[(3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthene]-3',6'-diyl)bis[(methylimino)-2,1-ethanediyl]]bis[2-iodo- (9CI) (CA INDEX NAME)



- CC 6-3 (General Biochemistry)
- ST rhodamine troponin complex **peptide** muscle fiber
conformation electrostatic force
- IT Troponins
(C; bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)
- IT Troponins
(I, switch **peptide** of troponin C; bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)
- IT Electrostatic force
Molecular association
(bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)
- IT Muscle
(fiber; bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)
- IT Protein motifs
(regulatory; bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)
- IT Self-association
(troponin C in complex with switch **peptide** of troponin I shows dimerization)
- IT 203580-70-5

(bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)

IT 7440-70-2, Calcium, biological studies
(bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)

IT 529505-78-0D, complexes with troponin C
(bifunctional rhodamine probes can be used to det. orientation and motion of regulatory domain of troponin C-switch **peptide** from troponin I complex without altering conformation of labeled domain)

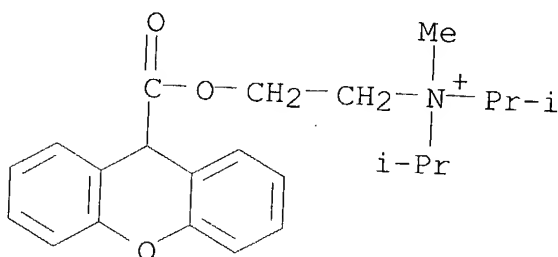
L99 ANSWER 3 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:395285 An improved method of evaluation of drug-evoked changes in gastric emptying in mice. Osinski, M. A.; Seifert, T. R.; Cox, B. F.; Gintant, G. A. (Department of Integrative Pharmacology, Abbott Laboratories, Abbott Park, IL, 60064-6119, USA). Journal of Pharmacological and Toxicological Methods, 47(2), 115-120 (English) 2002. CODEN: JPTMEZ. ISSN: 1056-8719. Publisher: Elsevier Science Inc..

AB The increased availability of transgenic mice prompts a need for the adaptation to mice of whole-animal assays traditionally performed in larger lab. animals. Gastric emptying studies are frequently conducted in dogs and rats. Mouse-based gastric emptying models currently available often use inert, nonnutrient liq. meals contg. nonabsorbable **markers** or **radionuclides**. We have developed a mouse gastric emptying assay that features a favorable throughput and the use of a semisolid, high-calorie meal. A carbohydrate- and **protein-rich semisolid test** meal was prepd. from common lab. reagents. Gastric emptying was detd. by subtracting the mass of test meal remaining in the stomach from the mass of test meal administered. A time-course study of basal emptying of a semisolid, paste-like test meal high in carbohydrate and protein from the stomachs of overnight-fasted mice was conducted. Agents known to either inhibit (propantheline, 0.3-10 mg/kg s.c.; corticotropin-releasing factor [CRF], 3-100 nmol/kg i.p.) or accelerate (metoclopramide, 1-10 mg/kg i.p.; bethanechol, 1-30 mg/kg i.p.) gastric emptying were tested. A single time-point variation of the assay can be used for quickly screening compds. for effects on gastric emptying. In time-course studies, the test meal emptied from the stomach with a half-emptying time of 30.6 min (95% CI: 27.3-34.7). The gastric emptying data were successfully modeled by a two-parameter exponential decay function. No lag phase was obsd., indicating that the meal empties from the stomach as a liq. The anticholinergic agent propantheline

increased gastric half-emptying time ($t_{1/2}$) approx. threefold, while metoclopramide decreased gastric half-emptying time approx. twofold compared to basal emptying. Single time-point screening studies correctly detected the gastrokinetic activity of bethanechol and the inhibitory effect of CRF. The mouse gastric emptying assay reported here is simple, inexpensive, and not labor-intensive. It is capable of detecting either stimulation or inhibition of gastric motor activity. This assay should prove useful for identifying drug-evoked changes in gastric emptying as well as for assessing the gastric motility effects of altered gene expression in genetically modified mice.

- IT 50-34-0, Propantheline bromide
(method for evaluation of drug-evoked changes in mice gastric emptying)
RN 50-34-0 HCA
CN 2-Propanaminium, N-methyl-N-(1-methylethyl)-N-[2-[(9H-xanthen-9-ylcarbonyl)oxy]ethyl]-, bromide (9CI) (CA INDEX NAME)



● Br⁻

- CC 1-1 (Pharmacology)
IT 50-34-0, Propantheline bromide 674-38-4, Bethanechol
7232-21-5, Metoclopramide hydrochloride
(method for evaluation of drug-evoked changes in mice gastric emptying)

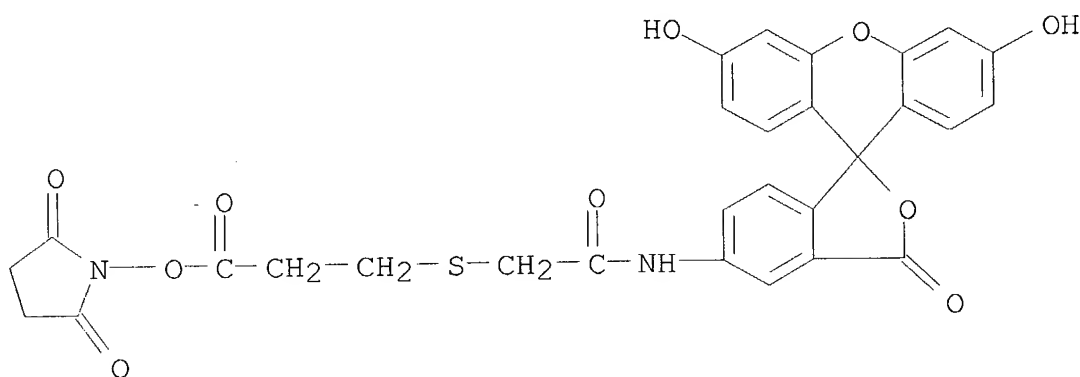
L99 ANSWER 4 OF 28 HCA COPYRIGHT 2004 ACS on STN
138:390922 Arsenide compound system for selective targeting of apoptotic cells. Hogg, Philip John (Unisearch Limited, Australia). PCT Int. Appl. WO 2003039564 A1 20030515, 85 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE,

BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English).
 CODEN: PIXXD2. APPLICATION: WO 2002-AU1523 20021108. PRIORITY: AU 2001-8746 20011108.

AB The invention discloses a method of selectively targeting an active agent (or agent capable of becoming an active agent) to apoptotic cells in a vertebrate, comprising administering to the vertebrate a system comprising an arsenoxide (or arsenoxide equiv.) compd. and the agent, wherein the system selectively targets apoptotic cells. Prepn. of e.g. 4-[N-(S-glutathionylacetyl)amino]phenylarsenoxide is described.

IT **123761-26-2**
 (arsenide compd. system for selective targeting of apoptotic cell)

RN 123761-26-2 HCA
 CN Acetamide, N-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)-2-[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]- (9CI) (CA INDEX NAME)



IC ICM A61K033-36
 ICS A61K047-04; A61P035-00; A61P019-00; A61P009-10

CC 63-6 (Pharmaceuticals)
 Section cross-reference(s): 1, 8, 9, 29

IT **Proteins**
 (RIP (ribosome-inactivating **protein**); arsenide compd. system for selective targeting of apoptotic cell)

IT Amines, biological studies
 Amino acids, biological studies
 Oligosaccharides, biological studies
Peptides, biological studies
Proteins

(conjugates; arsenide compd. system for selective targeting of apoptotic cell)

IT 37318-49-3, **Protein disulfide isomerase**
 (arsenide compd. system for selective targeting of apoptotic

cell)
IT 70-18-8, Glutathione, reactions 98-50-0, p-Arsanilic acid
598-21-0, Bromoacetyl bromide 89889-52-1 123761-26-2
(arsenide compd. system for selective targeting of apoptotic
cell)

L99 ANSWER 5 OF 28 HCA COPYRIGHT 2004 ACS on STN

137:381966 Methods and compositions for **analyzing**

proteins. Singh, Sharat; Salimi-Moosavi, Hossein; Tahir,
Syed Hasan; Wallweber, Gerald J.; Kirakossian, Hrair; Matray, Tracy
J.; Hernandez, Vincent S. (Aclara Biosciences, Inc., USA). PCT Int.
Appl. WO 2002095356 A2 20021128, 141 pp. DESIGNATED STATES: W: AE,
AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR,
CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU,
ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV,
MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD,
SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU,
ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ,
CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU,
MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN:
PIXXD2. APPLICATION: WO 2002-US16098 20020521. PRIORITY: US
2001-PV292548 20010521; US 2001-PV334901 20011024.

AB The invention concerns methods, compns. and kits are disclosed for
detg. one or more target **polypeptides** in a sample where
the target **polypeptides** have undergone a
post-translational modification. A mixt. comprising the sample and
a first reagent comprising a cleavage-inducing moiety and a first
binding agent for a binding site on a target **polypeptide**
is subjected to conditions under which binding of resp. binding
moieties occurs. The binding site is the result of
post-translational modification activity involving the target
polypeptide. The method may be employed to det. the target
polypeptide itself. In another embodiment the presence
and/or amt. of the target **polypeptide** is related to the
presence and/or amt. and/or activity of an agent such as an enzyme
involved in the post-translational modification of the target
polypeptide. The interaction between the first binding
agent and the binding site brings the cleavage-inducing moiety into
close proximity to a cleavable moiety, which is assocd. with the
polypeptide and is susceptible to cleavage only when in
proximity to the cleavage-inducing moiety. In this way, an
electrophoretic tag for each of the **polypeptides** may be
released. Released electrophoretic tags are sepd. and the presence
and/or amt. of the target **polypeptides** are detd. based on
the corresponding electrophoretic tags.

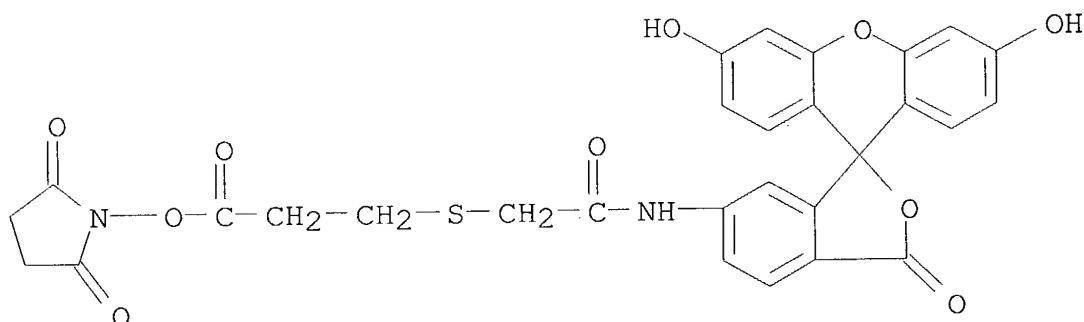
IT 331834-87-8P 476348-24-0P 476348-27-3P
476348-30-8P 476348-33-1P 476348-36-4P
476348-39-7P 476348-40-0P 476348-43-3P

476348-46-6P 476348-52-4P 476349-15-2P
 476360-19-7P 476360-20-0P 476360-21-1P
 476360-22-2P

(methods and compns. for analyzing proteins)

RN 331834-87-8 HCA

CN Acetamide, N-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-6-yl)-2-[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]- (9CI) (CA INDEX NAME)

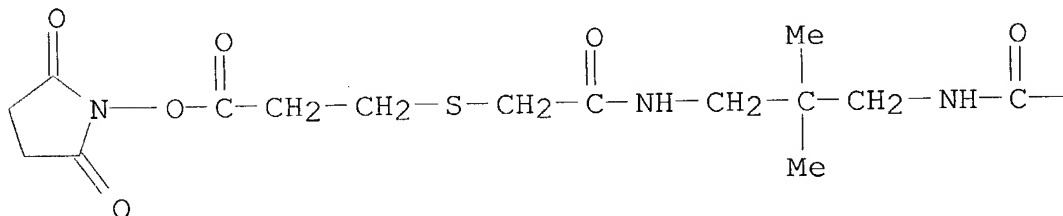


RN 476348-24-0 HCA

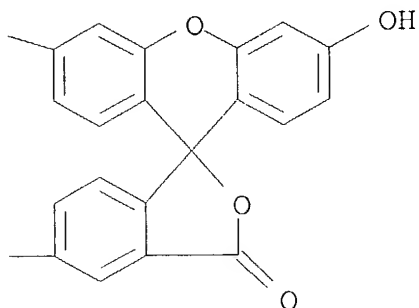
CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-5-carboxamide, N-[3-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]-2,2-dimethylpropyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A

HO—



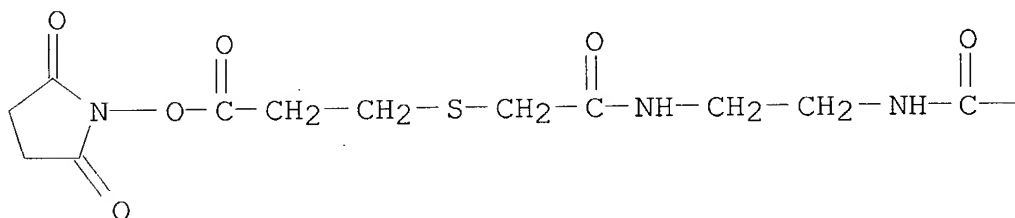
PAGE 1-B



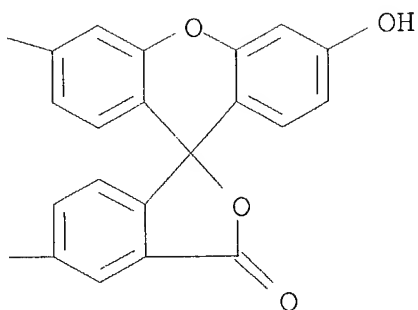
RN 476348-27-3 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
 N-[2-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]ethyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA
 INDEX NAME)

PAGE 1-A

HO—



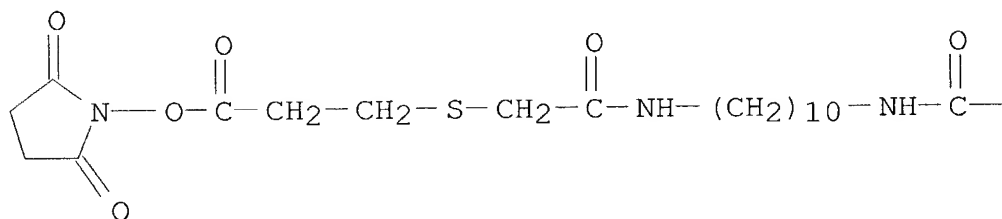
PAGE 1-B



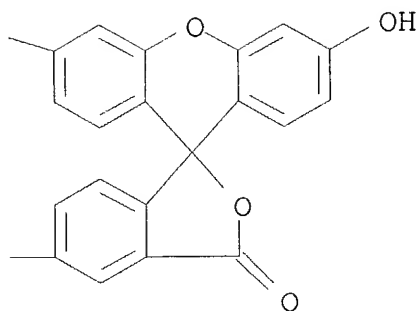
RN 476348-30-8 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
 N-[10-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]decyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A

HO—

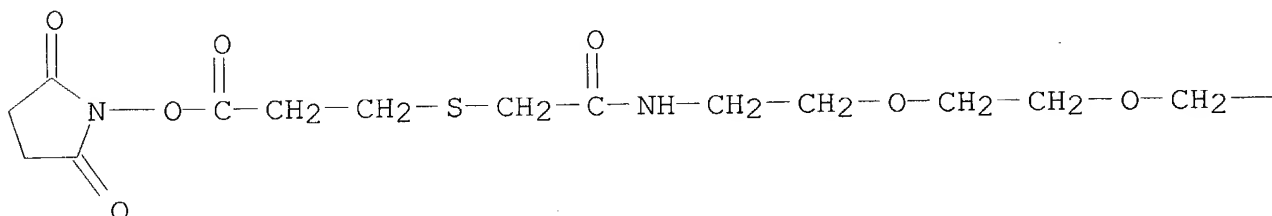


PAGE 1-B

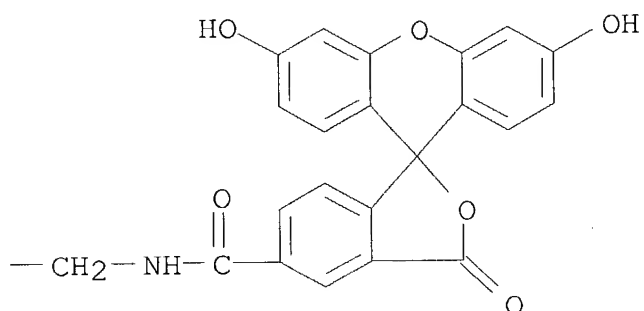


RN 476348-33-1 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
 N-[15-[(2,5-dioxo-1-pyrrolidinyl)oxy]-10,15-dioxo-3,6-dioxo-12-thia-9-azapentadec-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A

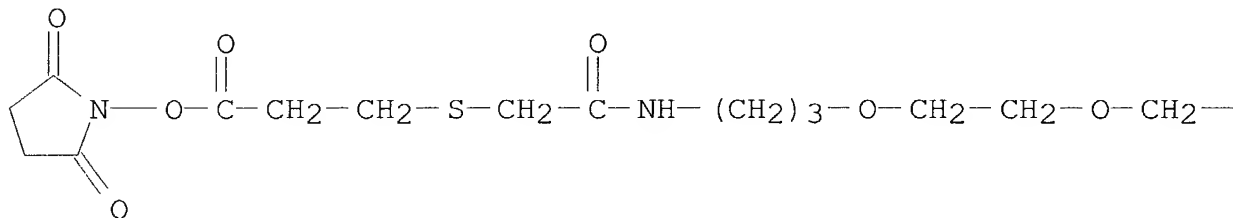


PAGE 1-B

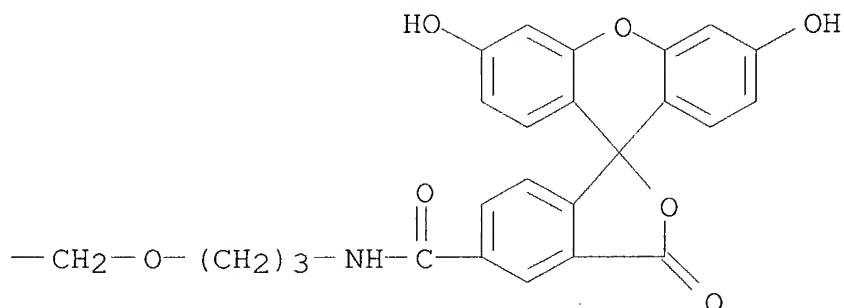


RN 476348-36-4 HCA
 CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-5-carboxamide,
 N-[20-[(2,5-dioxo-1-pyrrolidinyl)oxy]-15,20-dioxo-4,7,10-trioxa-17-
 thia-14-azaeicos-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A



PAGE 1-B

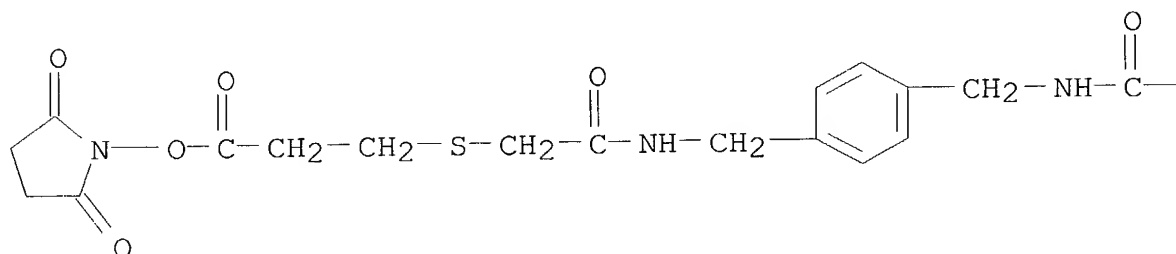


RN 476348-39-7 HCA

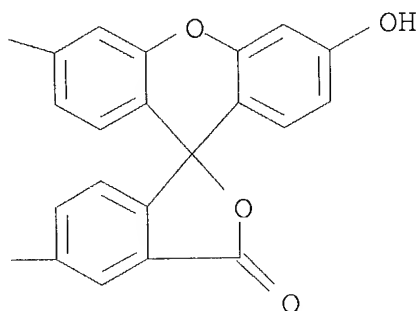
CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-5-carboxamide,
 N-[[4-[[[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]methyl]phenyl]methyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A

HO—



PAGE 1-B



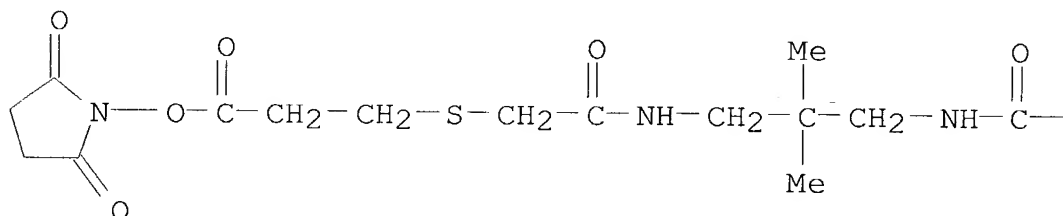
RN 476348-40-0 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-6-carboxamide,

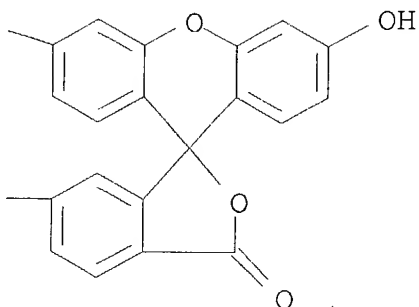
N-[3-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]-2,2-dimethylpropyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A

HO—



PAGE 1-B

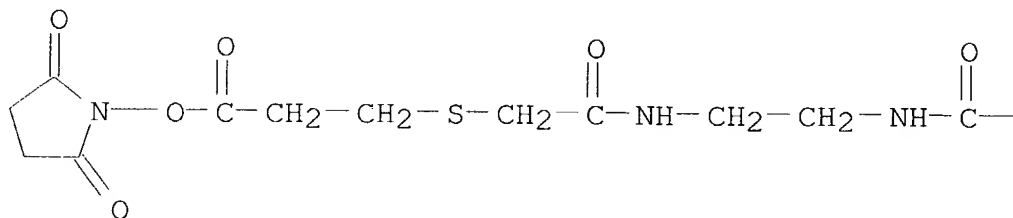


RN 476348-43-3 HCA

CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-6-carboxamide,
 N-[2-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]ethyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA
 INDEX NAME)

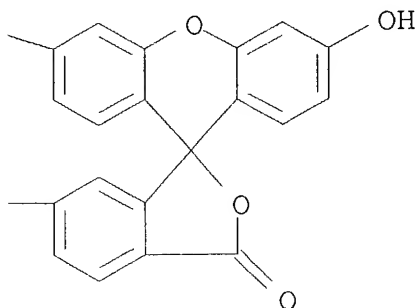
PAGE 1-A

HO—



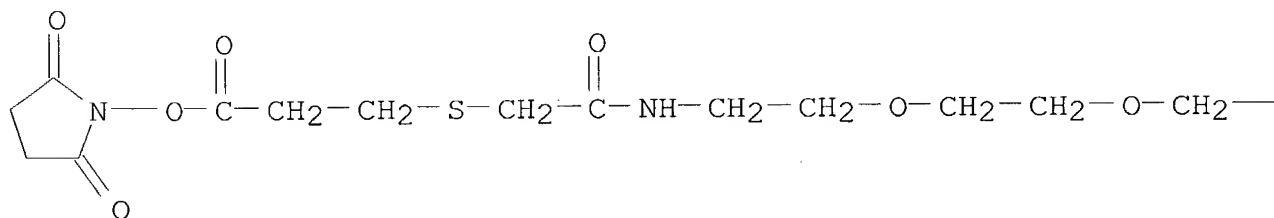


PAGE 1-B

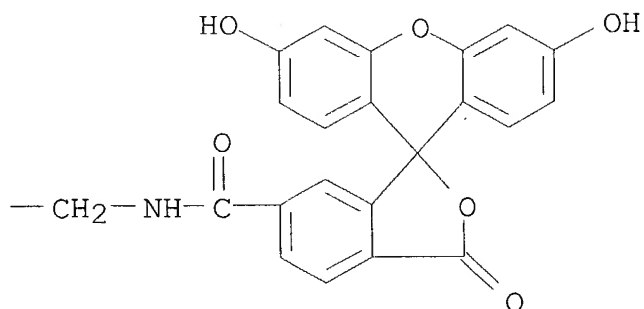


RN 476348-46-6 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-6-carboxamide,
 N-[15-[(2,5-dioxo-1-pyrrolidinyl)oxy]-10,15-dioxo-3,6-dioxa-12-thia-
 9-azapentadec-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A



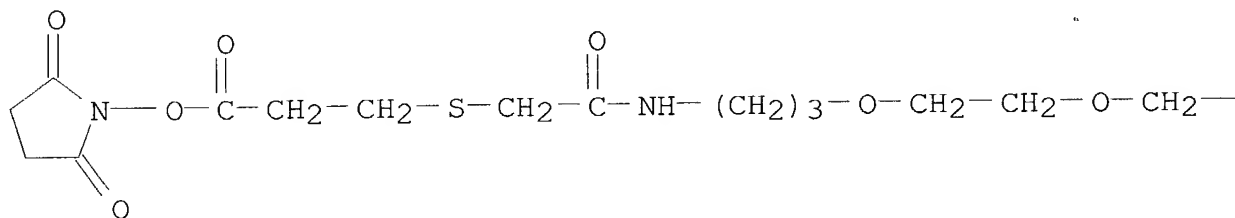
PAGE 1-B



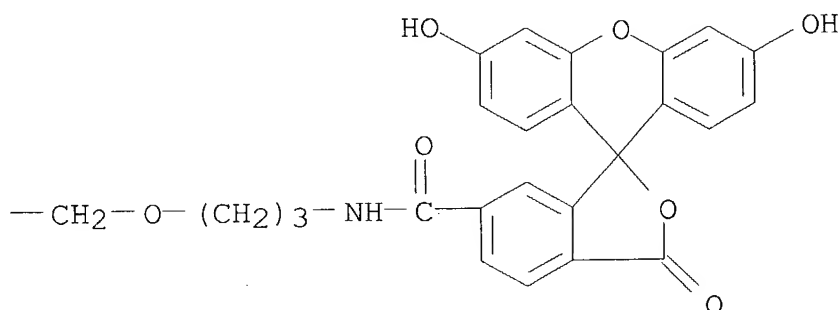
RN 476348-52-4 HCA

CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-6-carboxamide,
N-[20-[(2,5-dioxo-1-pyrrolidinyl)oxy]-15,20-dioxo-4,7,10-trioxa-17-
thia-14-azaeicos-1-yl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)

PAGE 1-A

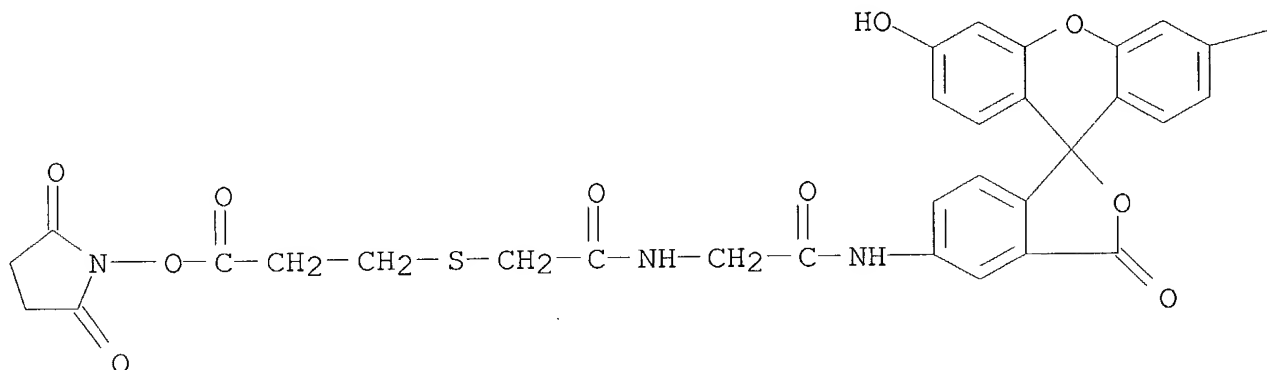


PAGE 1-B



RN 476349-15-2 HCA
CN Acetamide, N-[2-[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H), 9'-
[9H]xanthen]-5-yl)amino]-2-oxoethyl]-2-[[3-[(2,5-dioxo-1-
pyrrolidinyl)oxy]-3-oxopropyl]thio]- (9CI) (CA INDEX NAME)

PAGE 1-A



PAGE 1-B

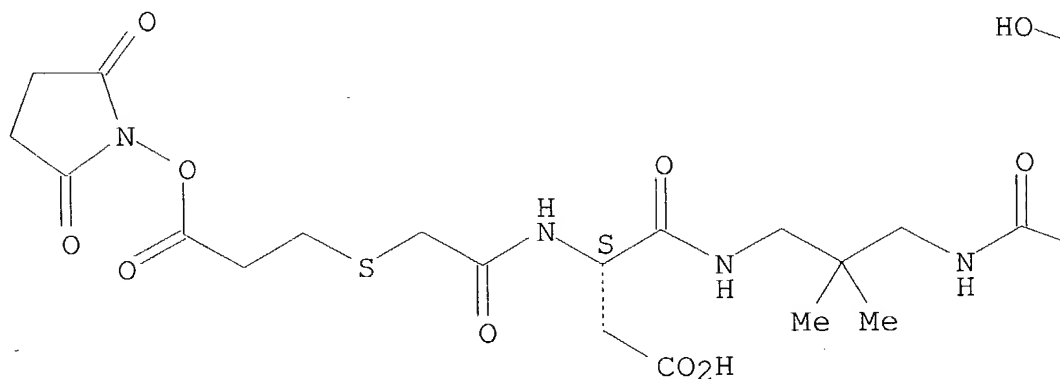
—OH

RN 476360-19-7 HCA
 CN Butanoic acid, 4-[[3-[[3'-(3,6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-6-yl)carbonyl]amino]-2,2-dimethylpropyl]amino]-3-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]-4-oxo-, (3S)- (9CI) (CA INDEX NAME)

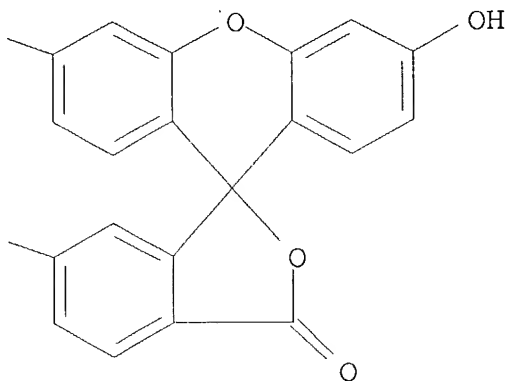
Absolute stereochemistry.

PAGE 1-A

HO—



PAGE 1-B



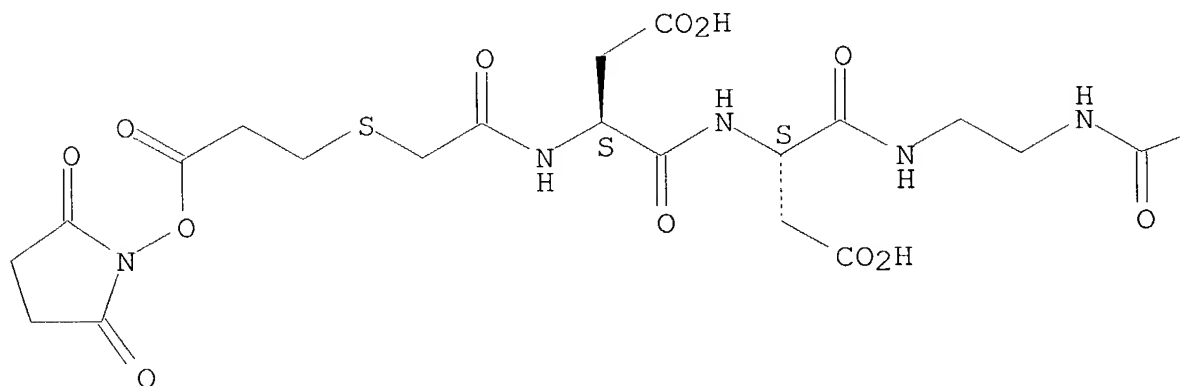
RN 476360-20-0 HCA

CN L-.alpha.-Asparagine, N-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]-L-.alpha.-aspartyl-N-[2-[[[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)carbonyl]amino]ethyl]- (9CI) (CA INDEX NAME)

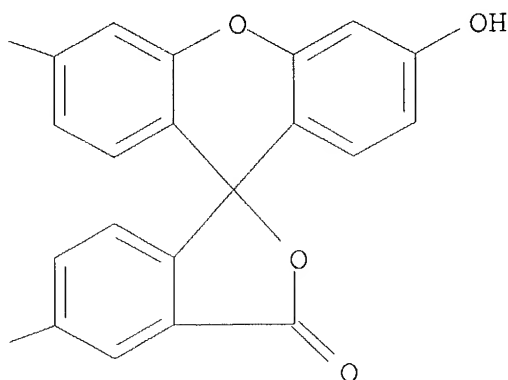
Absolute stereochemistry.

PAGE 1-A

HO—



PAGE 1-B

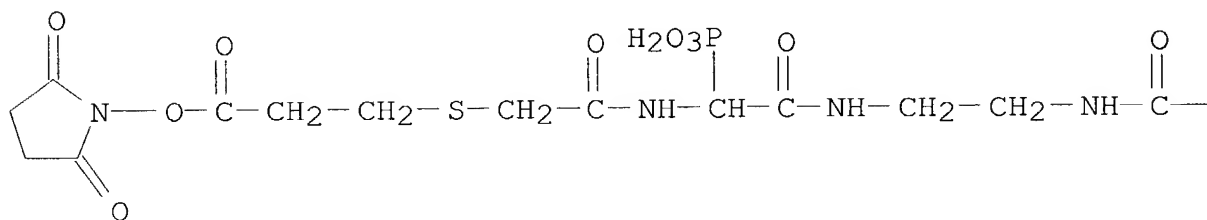


RN 476360-21-1 HCA

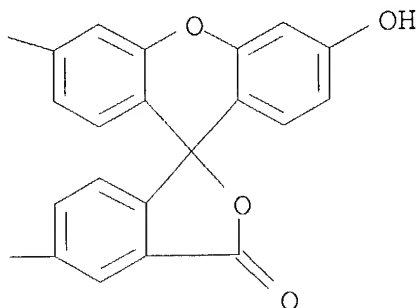
CN Phosphonic acid, [2-[[2-[[[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)carbonyl]amino]ethyl]amino]-1-[[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]acetyl]amino]-2-oxoethyl]-
(9CI) (CA INDEX NAME)

PAGE 1-A

HO—



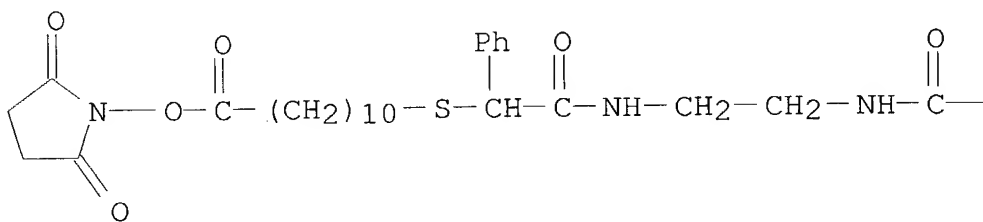
PAGE 1-B



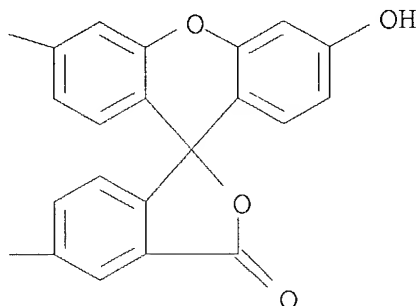
RN 476360-22-2 HCA
 CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
 N-[2-[[[11-[(2,5-dioxo-1-pyrrolidinyl)oxy]-11-oxoundecyl]thio]phenylacetyl]amino]ethyl]-3',6'-dihydroxy-3-oxo-
 (9CI) (CA INDEX NAME)

PAGE 1-A

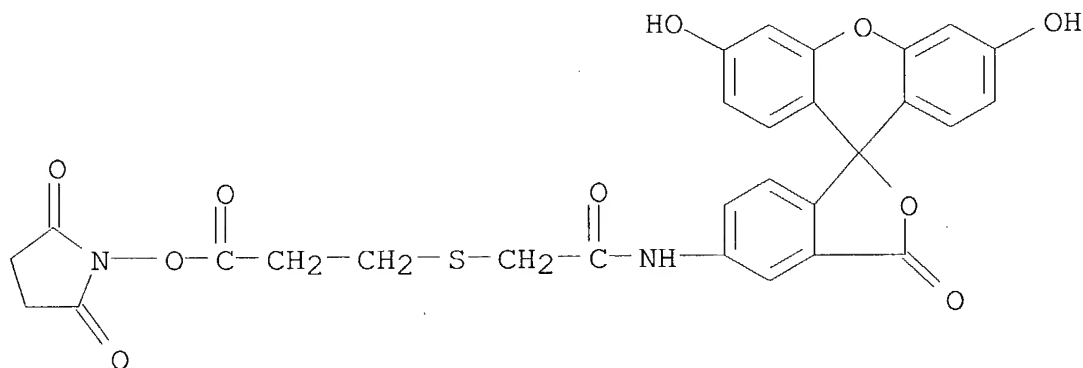
HO—



PAGE 1-B



IT 123761-26-2P
 (methods and compns. for **analyzing proteins**)
 RN 123761-26-2 HCA
 CN Acetamide, N-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)-2-[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]- (9CI) (CA INDEX NAME)



IC ICM G01N
 CC 9-16 (Biochemical Methods)
 Section cross-reference(s): 6
 ST phosphorylation **protein** chromatog reagent tags
 photosensitizer antibody immunoassay
 IT Immunoglobulins
 (G; methods and compns. for **analyzing proteins**)
 IT Antibodies
 (as electrophoretic probes, conjugated with e-tags; methods and compns. for **analyzing proteins**)
 IT Spheres
 (beads, photosensitizer; methods and compns. for **analyzing proteins**)

- IT Glycosylation
(biol.; methods and compns. for **analyzing proteins**)
- IT Enzymes, uses
(cofactors; methods and compns. for **analyzing proteins**)
- IT Ligands
(for **protein** receptors; methods and compns. for **analyzing proteins**)
- IT Affinity chromatography
(immobilized metal (IMAC); methods and compns. for **analyzing proteins**)
- IT Lipids, uses
(lipidation; methods and compns. for **analyzing proteins**)
- IT Acetylation
Acylation
Bond cleavage
Electrophoresis
Hydrolysis
Immunoassay
Isoprenylation
Methylation
Phosphate group
Phosphorylation, biological
Photosensitizers (pharmaceutical)
Ribosylation
Test kits
(methods and compns. for **analyzing proteins**)
- IT Cytokines
Peptides, analysis
(methods and compns. for **analyzing proteins**)
- IT Agglutinins and Lectins
(methods and compns. for **analyzing proteins**)
- IT Porphyrins
(methods and compns. for **analyzing proteins**)
- IT Reagents
(methods and compns. for **analyzing proteins**)
- IT Alkenes, properties
Thioethers
(methods and compns. for **analyzing proteins**)
- IT Receptors
(**protein**; methods and compns. for **analyzing proteins**)
- IT Ethers, properties
(seleno-; methods and compns. for **analyzing proteins**)
- IT Enzymes, uses

- (substrates; methods and compns. for analyzing proteins)
- IT Enzymes, uses
(subunits; methods and compns. for analyzing proteins)
- IT 58-85-5, Biotin 13780-71-7, Boronic acid
(contg.-moieties; methods and compns. for analyzing proteins)
- IT 150347-54-9
(methods and compns. for analyzing proteins)
- IT 331834-87-8P 476348-24-0P 476348-27-3P
476348-30-8P 476348-33-1P 476348-36-4P
476348-39-7P 476348-40-0P 476348-43-3P
476348-46-6P 476348-52-4P 476349-14-1P
476349-15-2P 476360-19-7P 476360-20-0P
476360-21-1P 476360-22-2P
(methods and compns. for analyzing proteins)
- IT 574-93-6, Phthalocyanine 2122-46-5, Phenoxy radical 3352-57-6,
Hydroxy radical, properties 7722-84-1, Hydrogen peroxide,
properties 11062-77-4, Superoxide anion
(methods and compns. for analyzing proteins)
- IT 81-88-9D, halogenated derivs. 2321-07-5D, Fluorescein, halogenated
derivs. 23627-89-6, Naphthalocyanine
(methods and compns. for analyzing proteins)
- IT 288-32-4, Imidazole, properties 288-42-6, Oxazole 288-47-1,
Thiazole
(methods and compns. for analyzing proteins)
- IT 63368-54-7P 73264-12-7P 106754-85-2P 106755-09-3P
123761-26-2P 136091-82-2P 148942-72-7P 476348-55-7P
476348-59-1P 476348-62-6P 476348-65-9P 476348-69-3P
476348-72-8P 476348-77-3P 476348-80-8P 476348-83-1P
476348-86-4P 476348-89-7P 476348-92-2P 476348-94-4P
476348-96-6P 476348-99-9P 476349-02-7P 476349-05-0P
476349-08-3P 476349-24-3P 476349-28-7P
(methods and compns. for analyzing proteins)
- IT 7782-44-7, Oxygen, properties
(singlet; methods and compns. for analyzing proteins)
- IT 60267-61-0, Ubiquitin
(ubiquitination; methods and compns. for analyzing proteins)

L99 ANSWER 6 OF 28 HCA COPYRIGHT 2004 ACS on STN ~

137:257647 Use of a substantially cell membrane impermeable arsenoxide compound for treating arthritis. Hogg, Philip John; Donoghue, Neil (Unisearch Limited, Australia). PCT Int. Appl. WO 2002074305 A1 20020926, 91 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ,

EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-AU310 20020319. PRIORITY: AU 2001-3798 20010319.

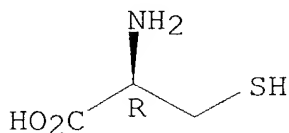
AB The invention provides a method of treatment and/or prophylaxis of arthritis in a vertebrate, comprising administering a therapeutically effective amt. of a compd. A-(L-Y)p [A = at least one substantially cell-membrane impermeable pendant group; L = linker and/or spacer group; Y = at least one arsenoxide or arsenoxide equiv.; p = 1-10; the sum total of carbon atoms in A and L together is greater than 6], or a pharmaceutically acceptable salt thereof, optionally together with a pharmaceutically acceptable carrier, diluent or excipient. Prepn. of compds. of the invention is described.

IT 52-90-4D, L-Cysteine, derivs.
(cell membrane impermeable arsenoxide compd. for treating arthritis)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

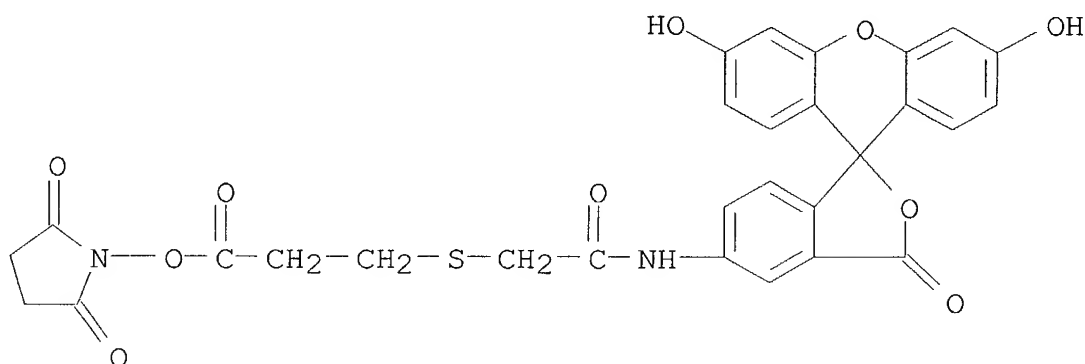
Absolute stereochemistry.



IT 123761-26-2 148356-00-7 148356-01-8
(reaction; cell membrane impermeable arsenoxide compd. for treating arthritis)

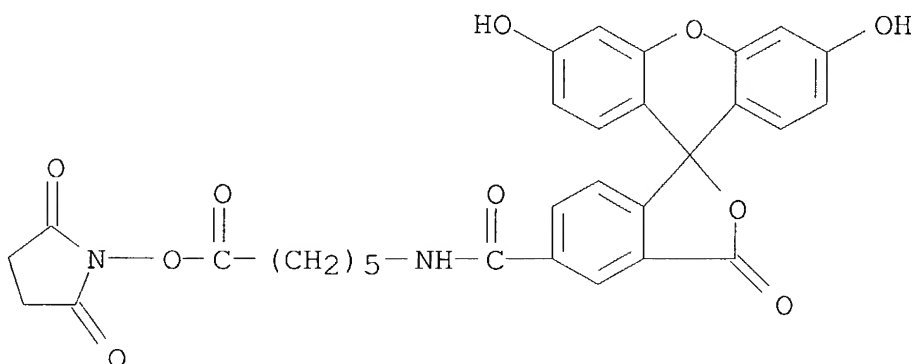
RN 123761-26-2 HCA

CN Acetamide, N-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)-2-[[3-[(2,5-dioxo-1-pyrrolidinyl)oxy]-3-oxopropyl]thio]- (9CI) (CA INDEX NAME)



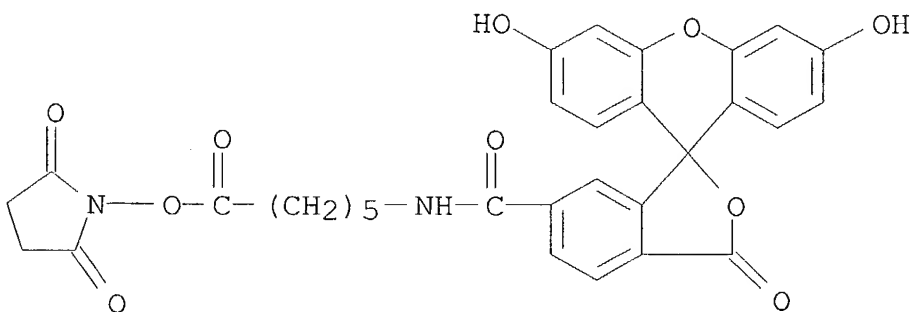
RN 148356-00-7 HCA

CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-5-carboxamide,
N-[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]-3',6'-dihydroxy-3-
oxo- (9CI) (CA INDEX NAME)



RN 148356-01-8 HCA

CN Spiro[isobenzofuran-1(3H), 9'-[9H]xanthene]-6-carboxamide,
N-[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]-3',6'-dihydroxy-3-
oxo- (9CI) (CA INDEX NAME)



- IC ICM A61K031-285
ICS A61P019-02
- CC 1-7 (Pharmacology)
Section cross-reference(s): 34, 63
- IT **Proteins**
(endothelial cell surface; cell membrane impermeable arsenoxide compd. for treating arthritis)
- IT Amines, biological studies
Amino acids, biological studies
Oligosaccharides, biological studies
Peptides, biological studies
Proteins
(linked arsenoxide derivs.; cell membrane impermeable arsenoxide compd. for treating arthritis)
- IT Sulfhydryl group
(**proteins** contg., linked arsenoxide derivs.; cell membrane impermeable arsenoxide compd. for treating arthritis)
- IT 59-52-9, 2,3,-Dimercapto-1-propanol 1077-28-7, 6,8-Thioctic acid 3483-12-3, Dithiothreitol 37318-49-3, **Protein disulfide isomerase** 117525-19-6 331722-91-9
(cell membrane impermeable arsenoxide compd. for treating arthritis)
- IT **52-90-4D, L-Cysteine**, derivs. 56-84-8D, L-Aspartic acid, linked arsenoxide derivs. 56-86-0D, L-Glutamic acid, linked arsenoxide derivs. 56-87-1D, L-Lysine, linked arsenoxide derivs. 58-85-5D, Biotin, linked arsenoxide derivs. 70-18-8D, Glutathione, derivs. 70-18-8D, Glutathione, linked arsenoxide derivs. 74-79-3D, L-Arginine, linked arsenoxide derivs. 498-40-8D, Cysteic acid, linked arsenoxide derivs. 2321-07-5D, Fluorescein, linked arsenoxide derivs. 3416-24-8D, Glucosamine, linked arsenoxide derivs. 19246-18-5D, derivs. 19246-18-5D, Cysteinylglycine, linked arsenoxide derivs. 172777-84-3D, Cy 5.5, linked arsenoxide derivs. 331815-00-0 331815-01-1 331815-02-2 331815-03-3 331815-04-4 331815-05-5 331815-06-6 331815-07-7 331815-08-8 331815-09-9 331815-10-2 463313-69-1 463313-70-4 463313-71-5
(cell membrane impermeable arsenoxide compd. for treating arthritis)
- IT 56-84-8, L-Aspartic acid, reactions 56-86-0, L-Glutamic acid, reactions 66-84-2, D-Glucosamine hydrochloride 70-18-8, Glutathione, reactions 98-50-0 107-96-0, 3-Mercaptopropanoic acid 498-40-8, L-Cysteic acid 598-21-0, Bromoacetyl bromide 6066-82-6, N-Hydroxysuccinimide 89889-52-1 **123761-26-2** **148356-00-7** **148356-01-8** 172777-84-3, Cy 5.5
(reaction; cell membrane impermeable arsenoxide compd. for treating arthritis)

L99 ANSWER 7 OF 28 HCA COPYRIGHT 2004 ACS on STN

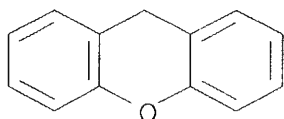
137:165832 Activity based probe analysis. Patricelli, Matthew P.
(Activx Biosciences, Inc., USA). PCT Int. Appl. WO 2002063271 A2
20020815, 62 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ,
BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ,
EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE,
KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW,
MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY,
DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT,
SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO
2002-US3808 20020205. PRIORITY: US 2001-PV266687 20010205.

AB The invention concerns methods and compns. are described for
analyzing complex protein mixts. using fluorescent
activity-based probes. In particular, probes that specifically
react with and bind to the active form of one or more target
proteins are employed. Fluorescent signals obtained from the
labeled active target proteins can be related to the presence or
amt. of active members of the desired target protein class. The
methods and compns. described herein can be used, for example, to
provide diagnostic information concerning pathogenic states, in
identifying proteins that may act as therapeutic
targets, and in drug discovery.

IT 92-83-1, Xanthene
(activity based probe anal.)

RN 92-83-1 HCA

CN 9H-Xanthene (9CI) (CA INDEX NAME)



IC ICM G01N

CC 9-14 (Biochemical Methods)
Section cross-reference(s): 1, 14

IT Capillary electrophoresis

Cyanine dyes

Diagnosis

Diffusion

Drug screening

Dyes

Electrophoresis apparatus

Fluorescent substances

Fluorometry

Functional groups

Gel electrophoresis

Labels

Mass spectrometry

Pathogen

Separation

(activity based probe anal.)

IT 91-64-5, Coumarin **92-83-1**, Xanthene 7440-18-8D,
Ruthenium, chelates 7440-27-9D, Terbium, chelates 7440-52-0D,
Erbium, chelates 25168-10-9, Naphthylamine 138026-71-8, BODIPY
(activity based probe anal.)

L99 ANSWER 8 OF 28 HCA COPYRIGHT 2004 ACS on STN

137:136908 Methods and means for detecting enzymatic cleavage and linkage reactions. Lopez-Calle, Eloisa; Fries, Joachim; Jungmann, Joern (Evotec OAI Ag, Germany). PCT Int. Appl. WO 2002059352 A2 20020801, 68 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (German). CODEN: PIXXD2. APPLICATION: WO 2002-EP845 20020128. PRIORITY: EP 2001-101869 20010126.

AB The invention relates to methods and means for detecting enzyme-catalyzed cleavage and linkage reactions. The invention provides modular chem. compds., which act as substrates for the enzymes concerned. The reaction products are detected using methods with a sensitivity to molar mass. Thus a Caspase 3-specific substrate was synthesized; first the substrate **peptide** was prepd. on a solid phase and coupled to 5-carboxytetramethylrhodamine succinimide ester. The product was modified with maleimide and conjugated to a 5'-thio modified double stranded DNA.

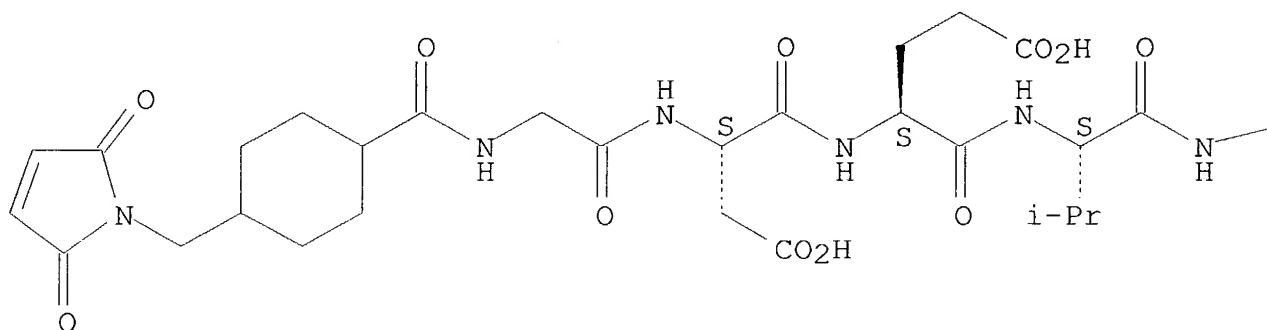
IT **444602-36-2P 444602-38-4P**
(methods and means for detecting enzymic cleavage and linkage reactions)

RN 444602-36-2 HCA

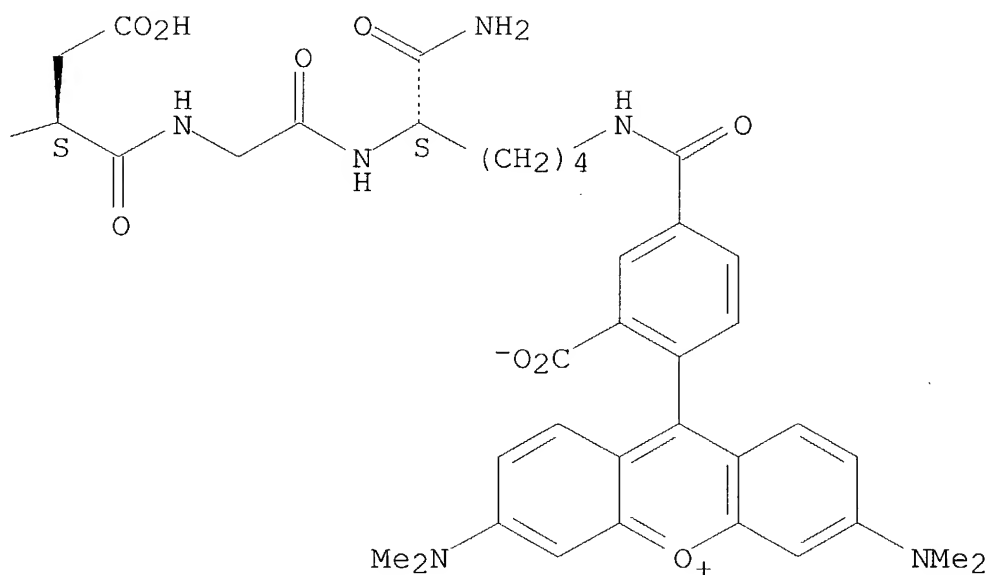
CN L-Lysinamide, N-[[4-[(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)methyl]cyclohexyl]carbonyl]glycyl-L-.alpha.-aspartyl-L-.alpha.-glutamyl-L-valyl-L-.alpha.-aspartylglycyl-N6-[4-[3,6-bis(dimethylamino)xanthylium-9-yl]-3-carboxybenzoyl]-, inner salt (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

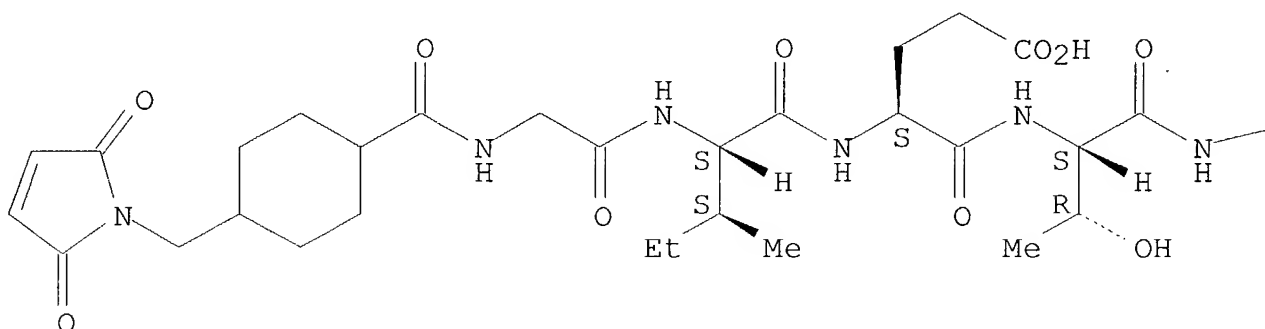


RN 444602-38-4 HCA

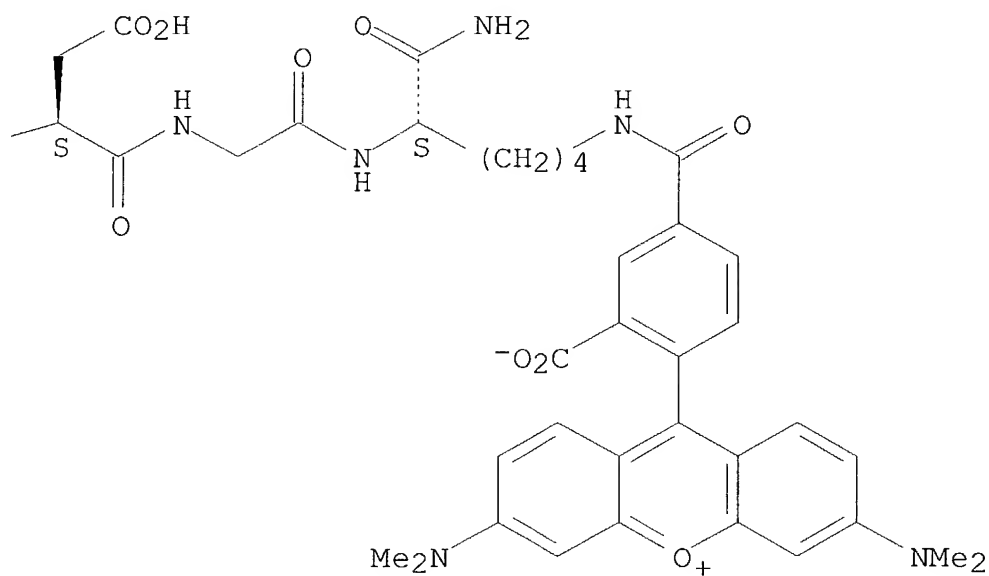
CN L-Lysinamide, N-[[4-[(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)methyl]cyclohexyl]carbonyl]glycyl-L-isoleucyl-L- α -glutamyl-L-threonyl-L- α -aspartylglycyl-N6-[4-[3,6-bis(dimethylamino)xanthylium-9-yl]-3-carboxybenzoyl]-, inner salt (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B



IC ICM C12Q001-37
 ICS C07K007-06
 CC 7-1 (Enzymes)
 Section cross-reference(s): 1
 IT Carbohydrates, biological studies
 Dendritic polymers
 Natural products
 Nucleic acids
Peptides, biological studies
 Polymers, biological studies

Proteins

(methods and means for detecting enzymic cleavage and linkage reactions)

IT 9000-83-3, ATPase 9000-92-4, Amylase 9001-62-1, Lipase
 9001-79-0, Phosphoamidase 9001-92-7, Protease 9012-56-0, Amidase
 9012-90-2, DNA-polymerase 9012-96-8, **Cysteine**
 desulphydrase 9013-05-2, Phosphatase 9013-18-7, Acyl-CoA
 synthetase 9014-19-1, Pyruvate carboxylase 9014-24-8,
 RNA-polymerase 9023-70-5, Glutamine synthetase 9024-52-6,
 Aldolase 9024-82-2, Pyrophosphatase 9026-81-7, Nuclease
 9027-22-9, Decarboxylase 9027-34-3 9031-55-4, Carboxylase
 9031-96-3, Peptidase 9032-92-2, Glycosidase 9044-86-4,
 Dehydratase 9047-25-0, Ammonia lyase 9068-67-1, Sulfatase
 169592-56-7, Caspase-3

(methods and means for detecting enzymic cleavage and linkage reactions)

IT 444196-89-8P 444196-90-1P 444196-91-2P 444196-92-3P
 444196-93-4P 444196-94-5P **444602-36-2P**
444602-38-4P

(methods and means for detecting enzymic cleavage and linkage reactions)

L99 ANSWER 9 OF 28 HCA COPYRIGHT 2004 ACS on STN

137:17446 Rhodamine fluorophore useful as labeling reagent. Quiarello, Ronald H.; Cheon, Liu Win; Yokobata, Kathy E. (Scinopharm Singapore Pte Ltd., Singapore). Jpn. Kokai Tokkyo Koho JP 2002168867 A2 20020614, 15 pp. (Japanese). CODEN: JKXXAF. APPLICATION: JP 2000-355808 20001122.

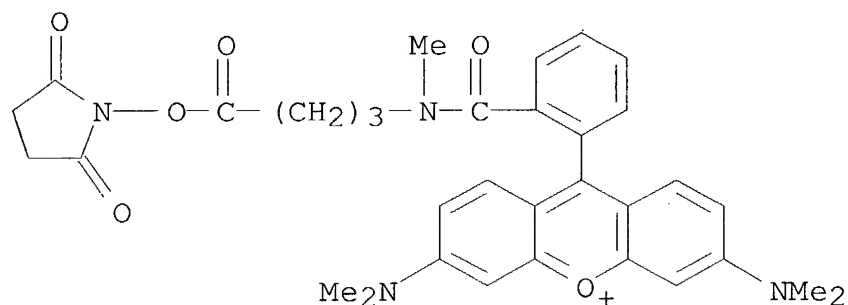
AB A Rhodamine fluorophore and its compn. useful as a labeling reagent is provided, with which a substance such as amino acid, **peptide, protein, nucleotide and nucleic acid** is inexpensively and conveniently labeled in a stable state without lowering an efficiency. A fluorescent substance based on Rhodamine is derivatized, which forms a label-bound body capable of generating fluorescence upon irradiating light with an appropriate wavelength. A particularly preferable example is a certain single isomer of Rhodamine phosphoramidite. With these Rhodamine phosphoramidites, the efficiency in synthesizing a Rhodamine-labeled compd. by a solid phase method is stimulated. In this example of label-bound body, the conversion to non-fluorescent lactam is prevented due to the possession of a sufficiently substituted amide linkage derived from 3-carboxylic acid.

IT **435304-72-6P 435304-73-7P**

(Rhodamine fluorophore useful as labeling reagent)

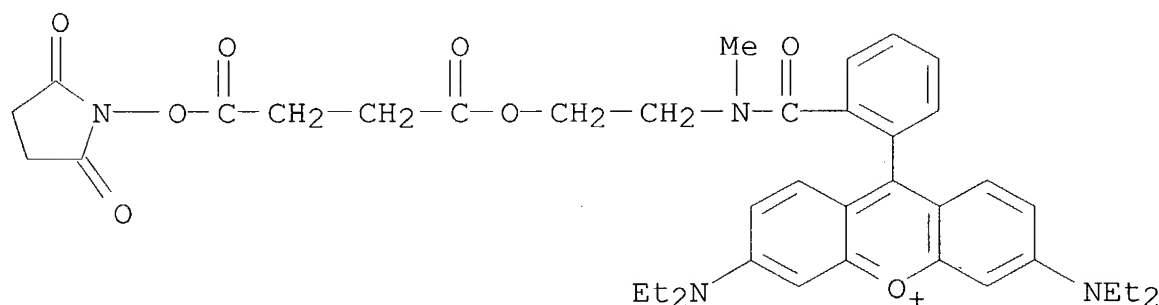
RN 435304-72-6 HCA

CN Xanthylum, 3,6-bis(dimethylamino)-9-[2-[[[4-[(2,5-dioxo-1-pyrrolidinyl)oxy]-4-oxobutyl]methylamino]carbonyl]phenyl]- (9CI)
 (CA INDEX NAME)



RN 435304-73-7 HCA

CN Xanthylium, 3,6-bis(diethylamino)-9-[2-[[[2-[4-[(2,5-dioxo-1-pyrrolidinyl)oxy]-1,4-dioxobutoxy]ethyl]methylamino]carbonyl]phenyl]-(9CI) (CA INDEX NAME)



IC ICM G01N033-533

ICS C12N015-09; C12Q001-02; C12Q001-68

CC 9-15 (Biochemical Methods)

IT Amide group

Amino group

Composition

Disulfide group

Fluorescence

Fluorescent substances

Light

Sulfhydryl group

Wavelength

(Rhodamine fluorophore useful as labeling reagent)

IT Amino acids, processes

Nucleic acids

Nucleotides, processes

Peptides, processes

Proteins

(Rhodamine fluorophore useful as labeling reagent)

IT 81-88-9DP, deriv. 81-88-9DP, phosphoramidite deriv.

13558-31-1DP, deriv. 13558-31-1DP, phosphoramidite deriv.

435304-66-8P 435304-67-9P 435304-68-0P 435304-69-1P

435304-70-4P 435304-71-5P **435304-72-6P**

435304-73-7P

(Rhodamine fluorophore useful as labeling reagent)

L99 ANSWER 10 OF 28 HCA COPYRIGHT 2004 ACS on STN

136:101105 Membrane binding **peptides** of CD59 and DAF

derivatives in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders. Rowling, Pamela Jane

Elizabeth; Smith, Geoffrey Paul; Ridley, Simon Hugh (Adprotech Limited, UK). PCT Int. Appl. WO 2002004638 A1 20020117, 51 pp.

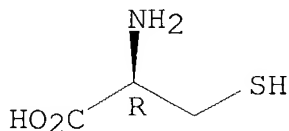
DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-GB3034 20010706. PRIORITY: GB 2000-16811 20000707.

AB The present invention provides membrane binding elements assocd. with a sol. deriv. of complement regulatory **polypeptides** CD59 or DAF that bind lipid raft components for delivery of compds. to lipid rafts to modulate intracellular or extracellular activity. Hence, this invention can be used in the treatment of inflammatory and other immune disorders. A sol. deriv. of CD59 or DAF is provided which is assocd. with two or more heterologous membrane binding **peptides** with low membrane affinity. These membrane binding elements are sol. in aq. soln., and the elements are capable of interacting, independently and with thermodyn. additivity with components of cellular or artificial membranes exposed to extracellular fluids. Specifically, the membrane binding elements target lipid raft components of the membrane and bind to the lipid rafts to localize the **polypeptide** at the lipid rafts. Thus, membrane binding elements mediate internalization of the **proteins**. Components of lipid rafts include one or more of phosphatidylserine, phosphatidyl glycerol, glycosphingolipids, cholesterol, GPI-anchored **proteins** assocd. with lipid rafts and other **protein** components of lipid rafts that may be found on the exo-plasmic cellular surface. Another embodiment of the invention provides sol. derivs. which include a derivatized antibody or antibody fragment which can provide a surrogate receptor localized at a lipid raft to divert a mediator interacting with a lipid raft receptor or which can neutralize a cofactor of the raft needed for signaling. Sol. derivs. also include chem. or biol. compds. that have fluorescent

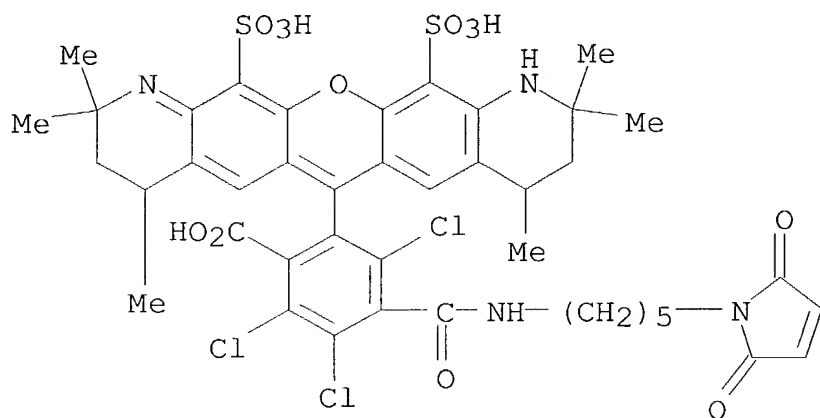
properties or compds. that can form chem. bonds with **proteins**, sugar groups or lipids with crosslinking groups, enzymes, enzyme substrates or inhibitors and are used to study patching behavior of membrane **proteins** and lipids in DIGs. Sol. **proteins** of the present invention can be linked to membrane binding elements by **disulfide** bonds. Sol. forms of **proteins** that are normally located in lipid rafts can be produced either by recombinant methods or isolated from human urine or plasma. These **proteins** can be treated with 2-iminothiolane and further reacted with a pyridylthio group linked to the membrane binding **peptide**. The membrane binding **peptide** may also be linked to the sol. **protein** by a C-terminal **cysteine** in the sol. **protein**.

- IT 52-90-4, **Cysteine**, biological studies
 (C-terminal, in CD59 and DAF **proteins**, for linkage to membrane **peptides**; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- RN 52-90-4 HCA
- CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



- IT 387847-69-0 387847-73-6 388621-69-0
 388621-72-5 388621-75-8
 (lipid-raft targeting using; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- RN 387847-69-0 HCA
- CN Benzoic acid, 2,3,5-trichloro-4-[[[5-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)pentyl]amino]carbonyl]-6-(1,3,4,8,9,10-hexahydro-2,2,4,8,10,10-hexamethyl-12,14-disulfo-2H-pyrano[3,2-g:5,6-g']diquinolin-6-yl)- (9CI) (CA INDEX NAME)

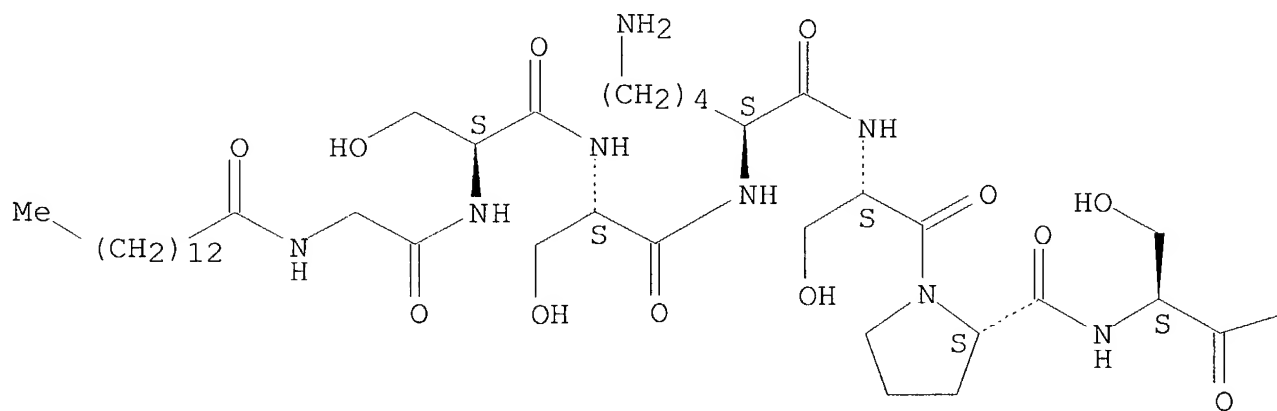


RN 387847-73-6 HCA

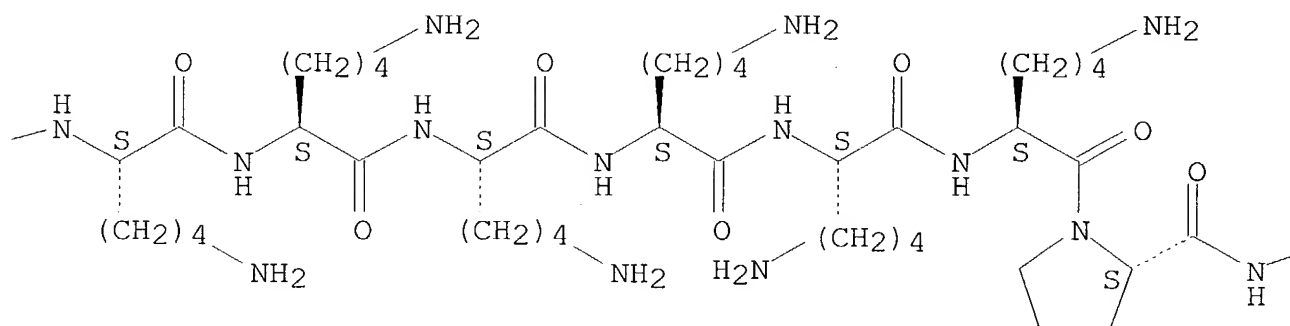
CN L-Cysteinamide, N-(1-oxotetradecyl)glycyl-L-seryl-L-seryl-L-lysyl-L-seryl-L-prolyl-L-seryl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-prolylglycyl-L-.alpha.-glutamyl-S-[1-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)-2,5-dioxo-3-pyrrolidinyl]-(9CI) (CA INDEX NAME)

Absolute stereochemistry.

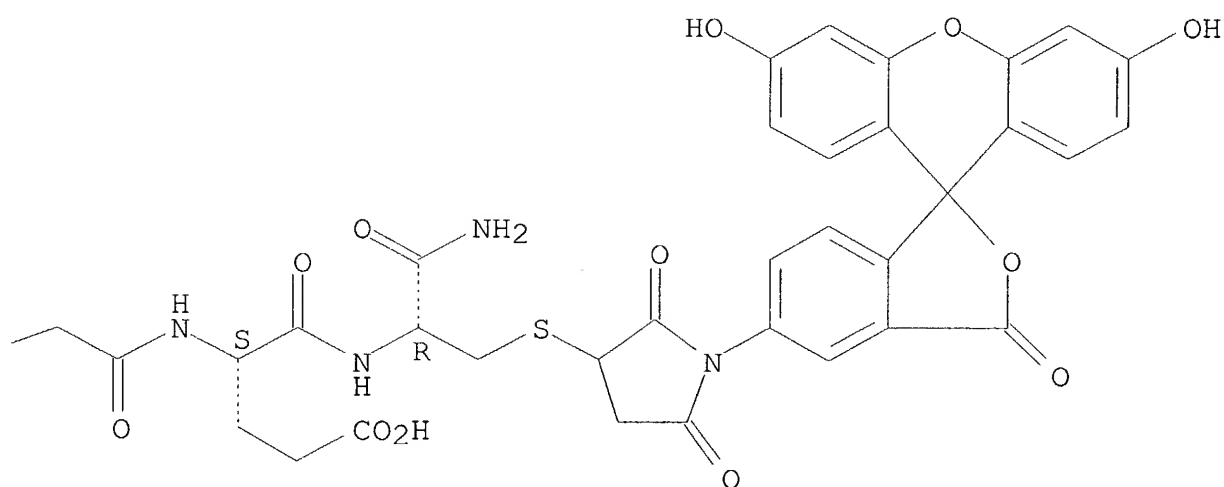
PAGE 1-A



PAGE 1-B

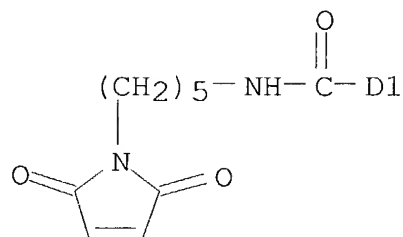
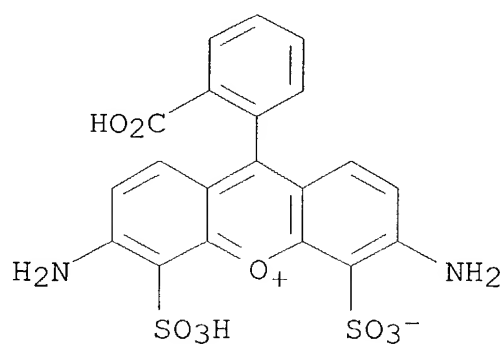


PAGE 1-C



RN 388621-69-0 HCA

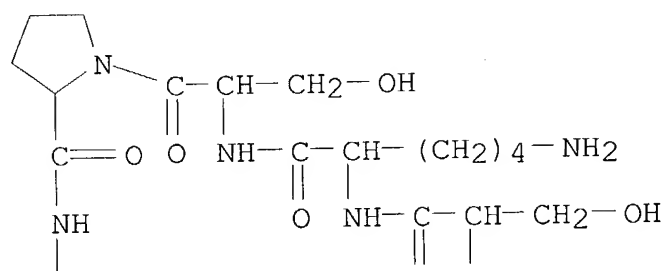
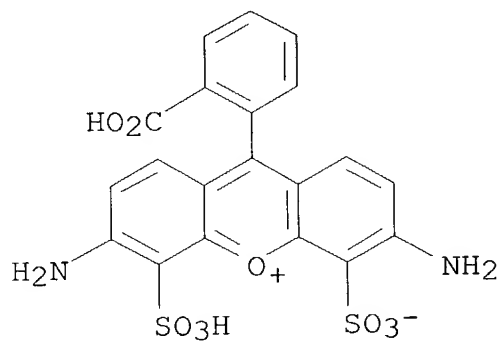
CN Xanthylum, 3,6-diamino-9-[2-carboxy-4(or 5)-[[[5-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)pentyl]amino]carbonyl]phenyl]-4,5-disulfo-, inner salt (9CI) (CA INDEX NAME)



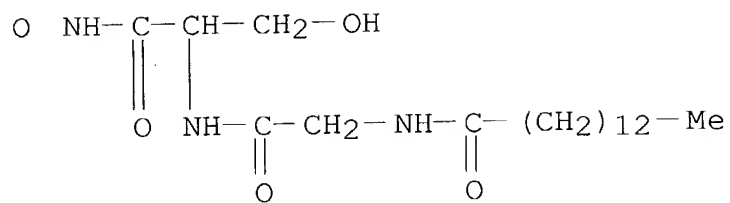
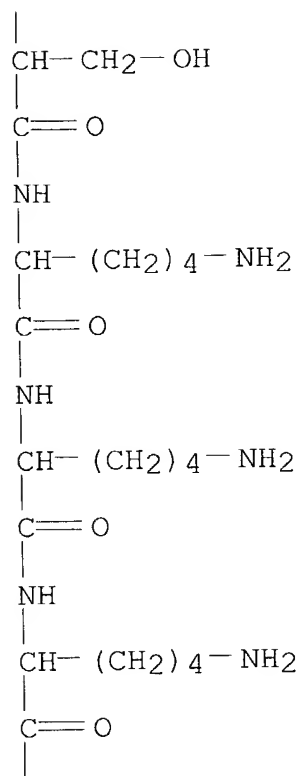
RN 388621-72-5 HCA

CN L-Cysteinamide, N-(1-oxotetradecyl)glycyl-L-seryl-L-seryl-L-lysyl-L-seryl-L-prolyl-L-seryl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-prolyl-glycyl-L-.alpha.-glutamyl-S-[1-[5-[[3(or 4)-carboxy-4(or 3)-(3,6-diamino-4,5-disulfoxanthylum-9-yl)benzoyl]aminopentyl]-2,5-dioxo-3-pyrrolidinyl]-, inner salt (9CI) (CA INDEX NAME)

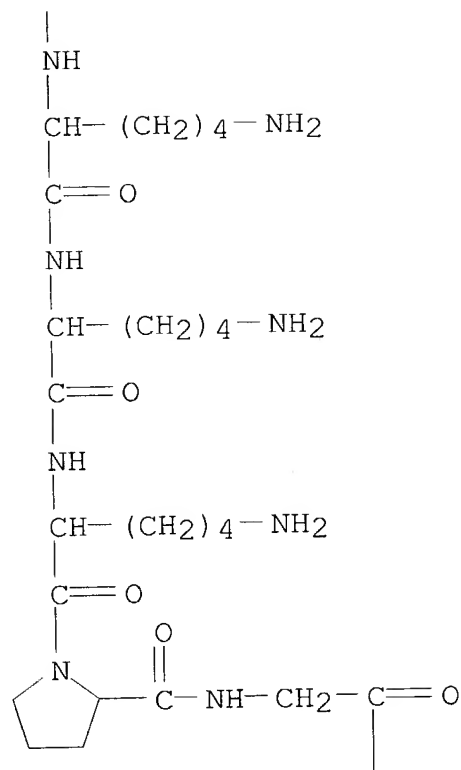
PAGE 1-A



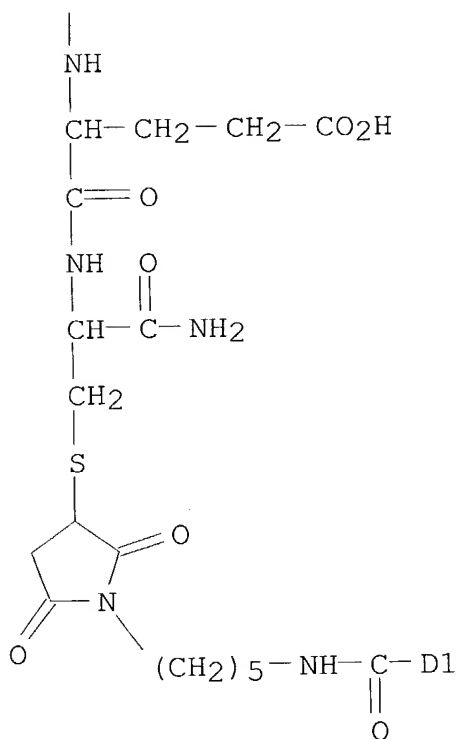
PAGE 2-A



PAGE 3-A



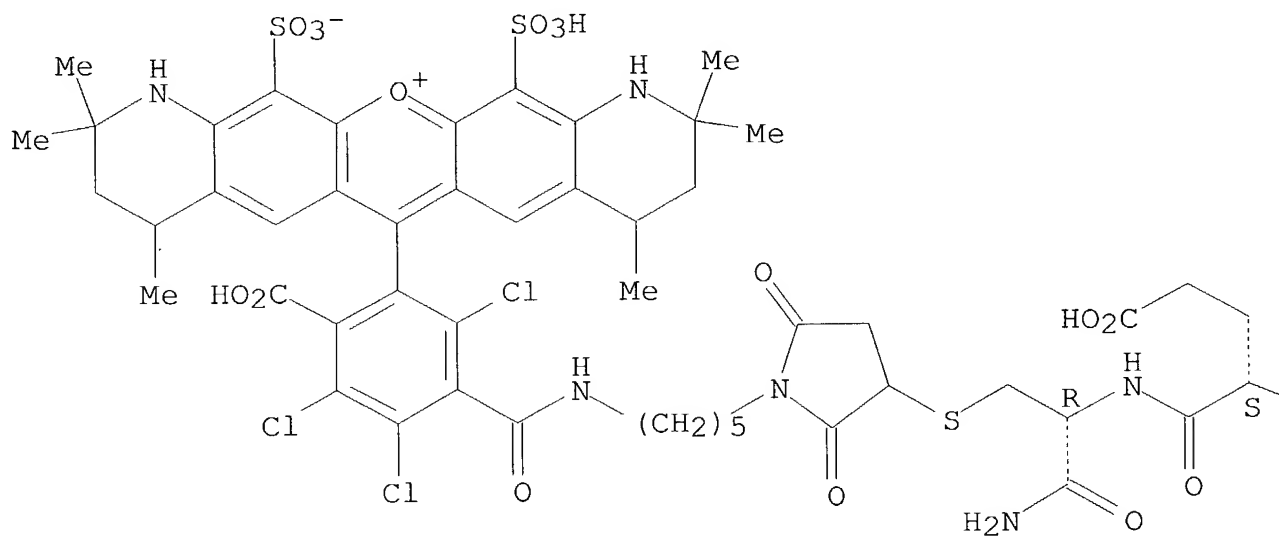
PAGE 4-A



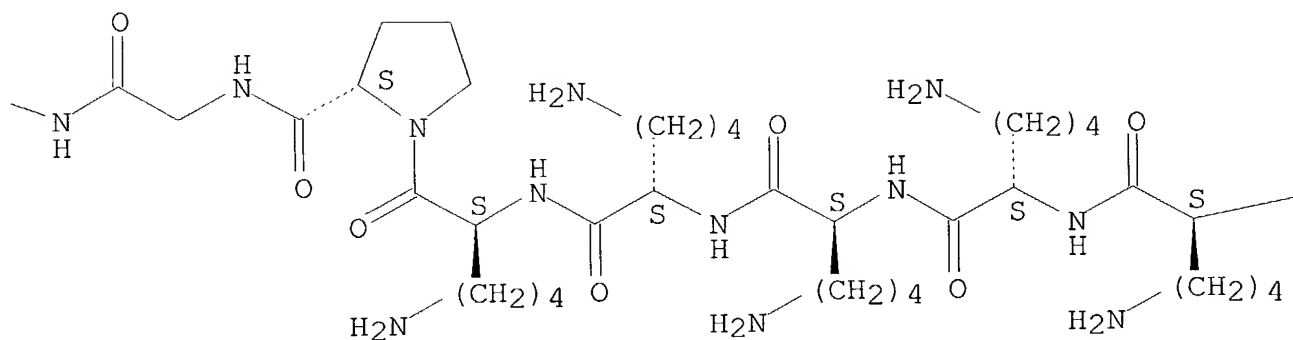
RN 388621-75-8 HCA
 CN L-Cysteinamide, N-(1-oxotetradecyl)glycyl-L-seryl-L-seryl-L-lysyl-L-seryl-L-prolyl-L-seryl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-lysyl-L-prolyl-glycyl-L- α -glutamyl-S-[1-[5-[[4-carboxy-2,3,6-trichloro-5-(1,2,3,4,8,9,10,11-octahydro-2,2,4,8,10,10-hexamethyl-12,14-disulfopyrano[3,2-g:5,6-g']diquinolin-13-ium-6-yl)benzoyl]amino]pentyl]-2,5-dioxo-3-pyrrolidinyl]-, inner salt (9CI) (CA INDEX NAME)

Absolute stereochemistry.

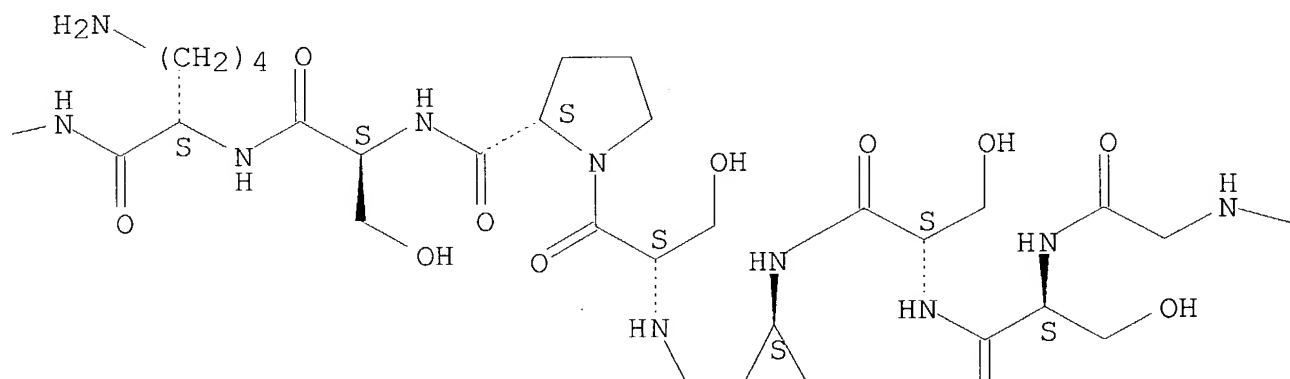
PAGE 1-A



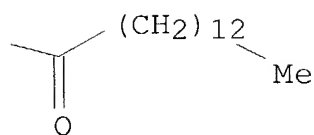
PAGE 1-B



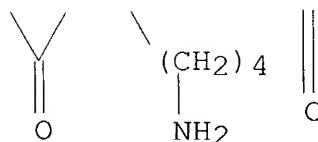
PAGE 1-C



PAGE 1-D



PAGE 2-C



IC ICM C12N015-12
 ICS C07K014-705; C07C323-41; C07C323-59; A61K047-48
 CC 15-4 (Immunochemistry)
 Section cross-reference(s): 3, 6, 14
 ST membrane binding **peptide** soluble complement regulator CD59
 DAF deriv; targeting lipid raft deriv CD59 DAF; treatment immune
 inflammatory disorder lipid raft deriv CD59 DAF; fusion
protein membrane binding **peptide** DAF; CD59 fusion
protein membrane binding **peptide**; CR1 receptor
 fusion **protein** membrane binding **peptide**
 IT Signal transduction, biological
 (CD59 and DAF derivs. in cell membrane lipid rafts in; membrane

- binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Carbohydrates, biological studies
- Lipids, biological studies
- Proteins**
- (CD59 and DAF **peptide** variants crosslinked by; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Brain
- (DAF from, human; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Glycosphingolipids
- Phosphatidylglycerols
- Phosphatidylserines
- (as lipid raft component; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders).
- IT Immunity
- (disorder, treatment of; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Crosslinking agents
- (enzyme-activated, covalent bonds with **proteins**, sugars or lipids in lipid rafts formed by; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Body fluid
- (extracellular, lipid rafts interacting with mols. from; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Chimeric gene
- (for CD59 and DAF fusion products with membrane binding **peptides**; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Urine
- (human, sol. CD59 from; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Enzymes, biological studies
- (inhibitors, lipid raft targeting using; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune

- disorders)
- IT Biological transport
(intracellular; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Confocal laser scanning microscopy
(lipid raft targeting visualized using; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Organelle
(lipid raft, in cell membrane; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Lysosome
(lipid raft-membrane targeting complexes in; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Fluorescence microscopy
(lipid raft-targeting complexes detected by; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Cell membrane
(membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Antibodies
(monoclonal, to CD59 or DAF derivs., fluorescent labeled, fragments of; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT **Protein** sequences
(of CD59 and DAF derivs. of human; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Post-translational processing
(of CD59 and DAF derivs. to link membrane binding **peptides**; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT **Protein** engineering
(of CD59 and DAF derivs.; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT Molecular cloning

(of CD59 and DAF sol. derivs.; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **Glycolipoproteins**

(phosphatidylinositol-contg., in lipid rafts; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **Crosslinking agents**

(photochem., covalent bonds with **proteins**, sugars or lipids in lipid rafts formed by; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **CD59 (antigen)**

(sol. derivs., fusion **proteins**, in lipid rafts;; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **Enzymes, biological studies**

(substrates for, lipid raft targeting using; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **Antibodies**

(to CD59 or DAF derivs., fluorescent labeled, fragments of; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **Inflammation**

(treatment of; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **Complement receptors**

(type 1, fusion **proteins**; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT **52-90-4, Cysteine, biological studies**

(C-terminal, in CD59 and DAF **proteins**, for linkage to membrane **peptides**; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

IT 388635-55-0 388635-56-1 388635-57-2 388635-58-3

(amino acid sequence; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)

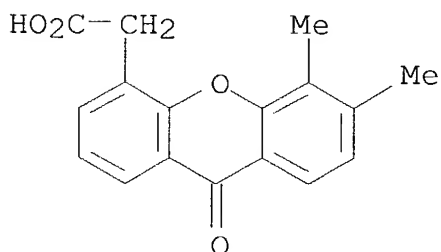
IT 57-88-5, Cholesterol, biological studies

- (as lipid raft component; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT 75350-46-8, Fluorescein-5-maleimide **387847-69-0**
387847-71-4 **387847-73-6** **388621-69-0**
388621-72-5 **388621-75-8**
(lipid-raft targeting using; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT 56-81-5, Glycerol, reactions 5961-85-3, Tris-2-carboxyethyl phosphine 6539-14-6, 2-Iminothiolane 143379-89-9
(sol. GPI **proteins** linked to membrane binding **peptides** using; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT 99085-47-9D, DAF, fusion **proteins**
(sol. derivs. of; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT 37758-47-7, Ganglioside GM1
(subunit B, as lipid-raft marker, fluorescent label on; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT 388649-87-4 388649-88-5 388649-89-6 388649-90-9 388649-91-0
388649-92-1
(unclaimed **protein** sequence; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- IT 202519-63-9
(unclaimed sequence; membrane binding **peptides** of CD59 and DAF derivs. in targeting lipid rafts of cell membranes for treatment of inflammatory and immune disorders)
- L99 ANSWER 11 OF 28 HCA COPYRIGHT 2004 ACS on STN
135:352306 Identification and reactivity of the major metabolite (.beta.-1-glucuronide) of the anti-tumor agent 5,6-dimethylxanthenone-4-acetic acid (DMXAA) in humans. Zhou, S. F.; Paxton, J. W.; Tingle, M. D.; Kestell, P.; Jameson, M. B.; Thompson, P. I.; Baguley, B. C. (Department of Pharmacology and Clinical Pharmacology, University of Auckland, Auckland, N. Z.). Xenobiotica, 31(5), 277-293 (English) 2001. CODEN: XENOBH. ISSN: 0049-8254. Publisher: Taylor & Francis Ltd..
- AB The novel antitumor agent 5,6-dimethylxanthenone-4-acetic acid (DMXAA) is extensively metabolized by glucuronidation and 6-methylhydroxylation, resulting in DMXAA acyl glucuronide (DMXAA-G) and 6-hydroxymethyl-5-methylxanthenone-4-acetic acid (6-OH-MXAA).

The major human urinary metabolite of DMXAA was isolated and purified by a solid-phase extn. (SPE) method. The isolated metabolite was hydrolyzed to free DMXAA by strong base, and by .beta.-glucuronidase. Liq. chromatog.-mass spectrometry (LC-MS) and spectral data indicated the presence of a mol. ion $[M + 1]^+$ at m/z 459, which was consistent with the mol. wt. of protonated DMXAA-G. The glucuronide was unstable in buffer at physiol. pH, plasma and blood with species variability in half-life. Hydrolysis and intramol. migration were major degrdn. pathways. In vitro and in vivo formation of DMXAA-protein adducts was obsd. The formation of DMXAA-protein adducts in cancer patients receiving DMXAA was significantly correlated with plasma DMXAA-G concn. and max. plasma DMXAA concn. At least five metabolites of DMXAA were obsd. in patient urine, with up to 60% of the total dose excreted as DMXAA-G, 5.5% as 6-OH-MXAA and 4.5% as the glucuronide of 6-OH-MXAA. These data suggest that the major metabolite in patients' urine is DMXAA .beta.-l-glucuronide, which may undergo hydrolysis, mol. rearrangement and covalent binding to plasma protein. The reactive properties of DMXAA-G may have important implications for the pharmacokinetics, pharmacodynamics and toxicity of DMXAA.

IT 117570-53-3D, 5,6-Dimethylxanthenone-4-acetic acid, protein adducts 162070-60-2, 5,6-Dimethylxanthenone-4-acetic acid acyl glucuronide 162070-60-2D, 5,6-Dimethylxanthenone-4-acetic acid acyl glucuronide isomer, protonated metabolite 223261-32-3, 6-Hydroxymethyl-5-methylxanthenone-4-acetic acid 372941-08-7, 6-Hydroxymethyl-5-methylxanthenone-4-acetic acid glucuronide 372941-08-7D, protonated metabolite (identification and reactivity of the major metabolite of the antitumor agent 5,6-dimethylxanthenone-4-acetic acid in humans)

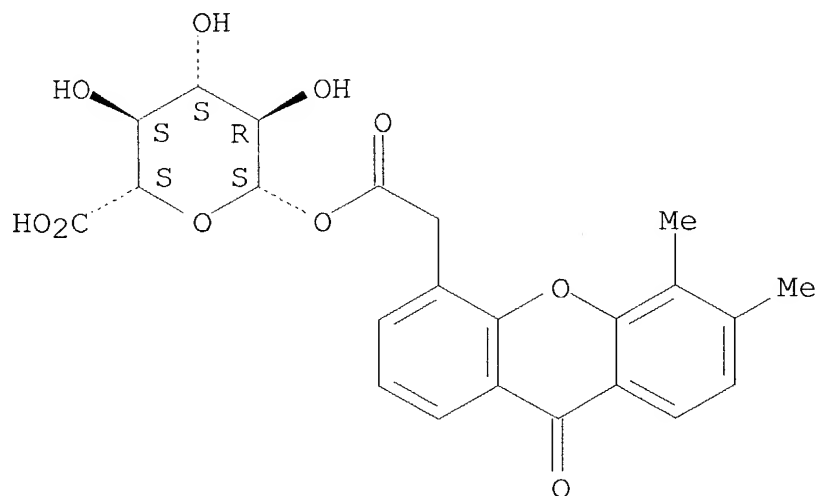
RN 117570-53-3 HCA
CN 9H-Xanthene-4-acetic acid, 5,6-dimethyl-9-oxo- (9CI) (CA INDEX NAME)



RN 162070-60-2 HCA
CN .beta.-D-Glucopyranuronic acid, 1-(5,6-dimethyl-9-oxo-9H-xanthene-4-

acetate) (9CI) (CA INDEX NAME)

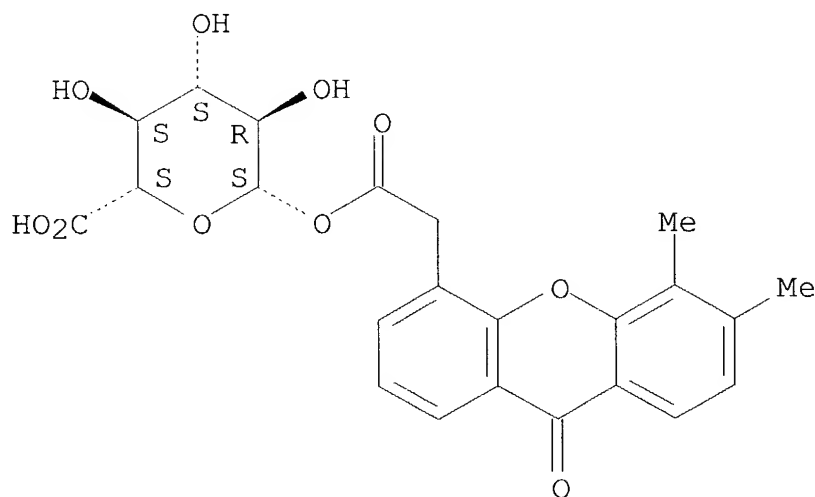
Absolute stereochemistry.



RN 162070-60-2 HCA

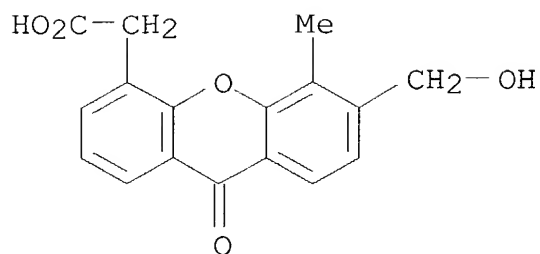
CN .beta.-D-Glucopyranuronic acid, 1-(5,6-dimethyl-9-oxo-9H-xanthene-4-acetate) (9CI) (CA INDEX NAME)

Absolute stereochemistry.



RN 223261-32-3 HCA

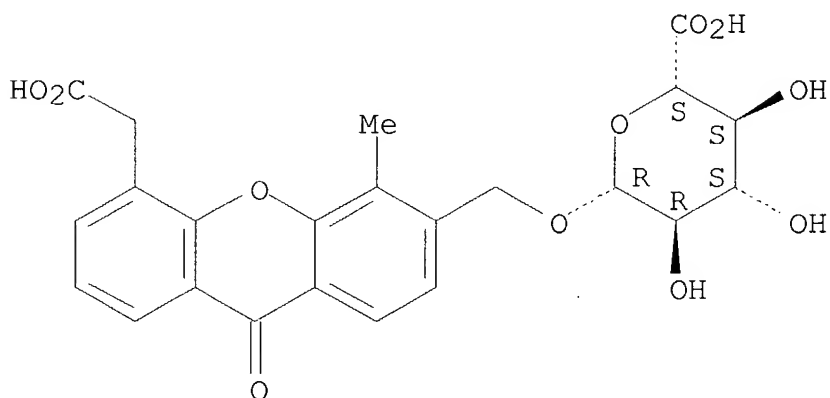
CN 9H-Xanthene-4-acetic acid, 6-(hydroxymethyl)-5-methyl-9-oxo- (9CI)
(CA INDEX NAME)



RN 372941-08-7 HCA

CN .beta.-D-Glucopyranosiduronic acid, [5-(carboxymethyl)-4-methyl-9-oxo-9H-xanthen-3-yl]methyl (9CI) (CA INDEX NAME)

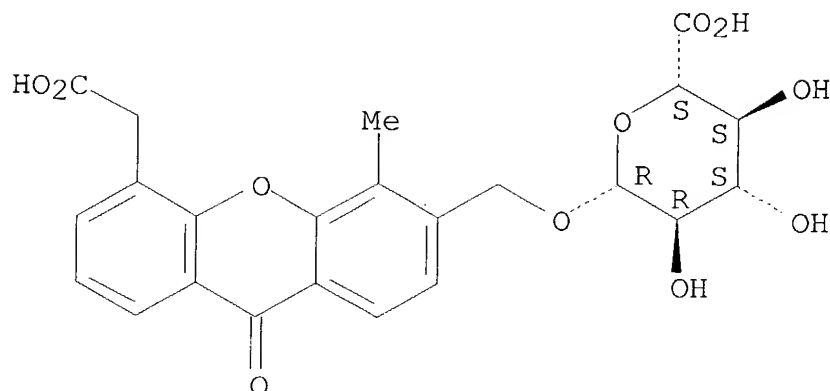
Absolute stereochemistry.



RN 372941-08-7 HCA

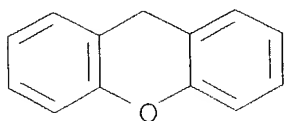
CN .beta.-D-Glucopyranosiduronic acid, [5-(carboxymethyl)-4-methyl-9-oxo-9H-xanthen-3-yl]methyl (9CI) (CA INDEX NAME)

Absolute stereochemistry.



- CC 1-2 (Pharmacology)
- IT **117570-53-3D**, 5,6-Dimethylxanthene-4-acetic acid, protein adducts **162070-60-2**, 5,6-Dimethylxanthene-4-acetic acid acyl glucuronide **162070-60-2D**, 5,6-Dimethylxanthene-4-acetic acid acyl glucuronide isomer, protonated metabolite **223261-32-3**, 6-Hydroxymethyl-5-methylxanthene-4-acetic acid **372941-08-7**, 6-Hydroxymethyl-5-methylxanthene-4-acetic acid glucuronide **372941-08-7D**, protonated metabolite (identification and reactivity of the major metabolite of the antitumor agent 5,6-dimethylxanthene-4-acetic acid in humans)
- L99 ANSWER 12 OF 28 HCA COPYRIGHT 2004 ACS on STN
- 135:238927 Silver and gold colloidal particle coating based optical sensors for biomolecule detection. Carron, Keith T.; Corcoran, Robert C.; Sulk, Roberta A. (University of Wyoming, USA). PCT Int. Appl. WO 2001071353 A1 20010927, 75 pp. DESIGNATED STATES: W: CA, JP, MX; RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US6357 20010228. PRIORITY: US 2000-527226 20000316.
- AB A colloidal system for detection of a variety of analytes is described which involves techniques which permit reconstitution of a desiccated substance such as for surface enhanced Raman spectroscopic anal. and multiple sensors at once, each having different spectra through the use of markers or the like. Competitive assay techniques and a variety of substances are described which provides a practical and versatile system which can also be used for immunol. assays and can include antibodies tagged to provide spectroscopic indicia.
- IT **92-83-1**, Xanthene (silver and gold colloidal particle coating based optical sensors for biomol. detection)

RN 92-83-1 HCA
 CN 9H-Xanthene (9CI) (CA INDEX NAME)



IC ICM G01N033-543
 CC 9-1 (Biochemical Methods)
 Section cross-reference(s): 2, 4, 15
 IT Alcohols, analysis
 Hormones, animal, analysis
 Neurotransmitters
 Phenols, analysis
 Prostate-specific antigen
Proteins, general, analysis
 (silver and gold colloidal particle coating based optical sensors
 for biomol. detection)
 IT **Polyoxyalkylenes, uses**
 (silver and gold colloidal particle coating based optical sensors
 for biomol. detection)
 IT 84-65-1, Anthraquinone 91-64-5, Coumarin **92-83-1**,
 Xanthene 94-75-7, 2,4-Dichlorophenoxyacetic acid, uses 574-93-6,
 Phthalocyanine 574-93-6D, Phthalocyanine, derivs. 1563-66-2,
 Carbofuran
 (silver and gold colloidal particle coating based optical sensors
 for biomol. detection)
 IT 7664-38-2D, phosphoric acid, derivs., uses 7664-93-9, Sulfuric
 acid, uses 9002-84-0, Teflon 13598-36-2D, phosphonic acid,
 derivs. 25322-68-3, **Polyethylene glycol**
 (silver and gold colloidal particle coating based optical sensors
 for biomol. detection)

L99 ANSWER 13 OF 28 HCA COPYRIGHT 2004 ACS on STN
 134:261272 Cell membrane-impermeable arsenoxide compounds, their
 preparation, pharmaceutical compositions, and therapeutic and
 diagnostic use. Hogg, Philip John; Donoghue, Neil (Unisearch
 Limited, Australia). PCT Int. Appl. WO 2001021628 A1 20010329, 122
 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG,
 BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB,
 GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
 LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL,
 PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US,
 UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE,
 BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE,
 IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN:

PIXXD2. APPLICATION: WO 2000-AU1143 20000920. PRIORITY: AU 1999-2967 19990920.

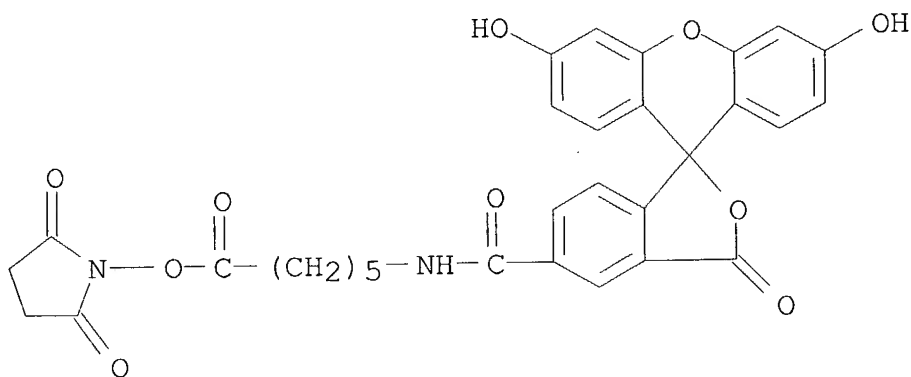
AB The invention discloses compds. A(LY)p, (A = .gtoreq.1 substantially cell-membrane impermeable pendant group; L = linker and/or spacer; Y = .gtoreq.1 arsenoxide or arsenoxide equiv.; p = 1-10; sum total of C atoms in A and L together >6). Prepn. of e.g. 4-[N-(S-glutathionylacetyl)amino]phenylarsenoxide is described, as are e.g. the antitumor activity, tumor imaging ability, and activity inhibiting HIV infection of compds. of the invention. Pharmaceutical formulations are also described.

IT 148356-00-7 148356-01-8

(reaction; substantially cell membrane-impermeable compd. and use thereof)

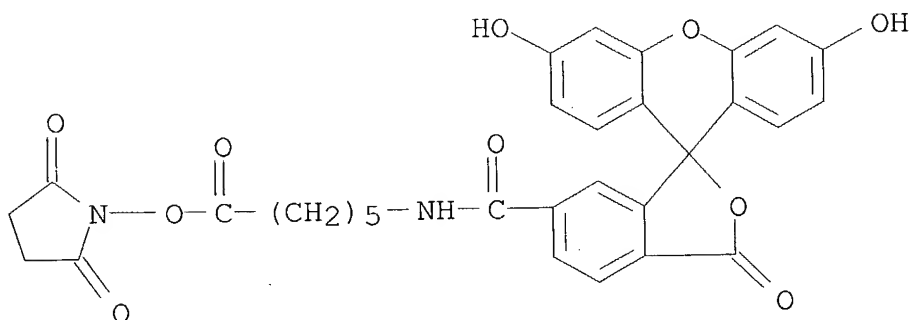
RN 148356-00-7 HCA

CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-5-carboxamide, N-[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)



RN 148356-01-8 HCA

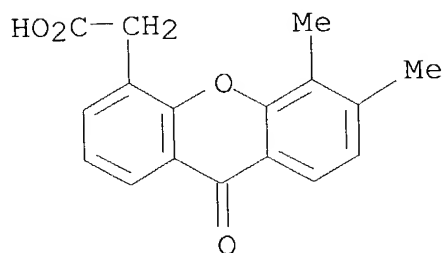
CN Spiro[isobenzofuran-1(3H),9'-[9H]xanthene]-6-carboxamide, N-[6-[(2,5-dioxo-1-pyrrolidinyl)oxy]-6-oxohexyl]-3',6'-dihydroxy-3-oxo- (9CI) (CA INDEX NAME)



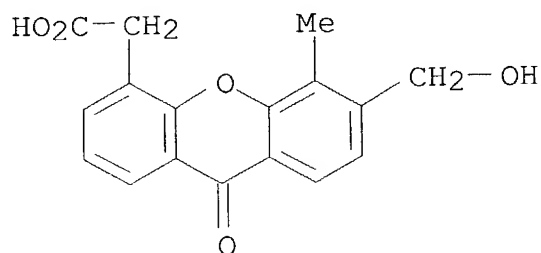
- IC ICM C07F009-20
ICS C07F009-78; C07F009-74
- CC 1-12 (Pharmacology)
Section cross-reference(s): 29, 63
- IT Amines, biological studies
Amino acids, biological studies
Oligosaccharides, biological studies
Peptides, biological studies
Proteins, general, biological studies
Radionuclides, biological studies
Transition metals, biological studies
(arsenoxide derivs.; substantially cell membrane-impermeable compd. and use thereof)
- IT Proteins, specific or class
(mercapto-contg., arsenoxide derivs.; substantially cell membrane-impermeable compd. and use thereof)
- IT 56-84-8, L-Aspartic acid, reactions 56-86-0, L-Glutamic acid, reactions 66-84-2, D-Glucosamine hydrochloride 70-18-8, Glutathione, reactions 98-50-0, p-Arsanilic acid 107-96-0, 3-Mercaptopropanoic acid 498-40-8, L-Cysteic acid 598-21-0, Bromoacetyl bromide 6066-82-6, N-Hydroxysuccinimide 67278-31-3 89889-52-1 123740-08-9 148356-00-7 148356-01-8 172777-84-3, Cy5.5
(reaction; substantially cell membrane-impermeable compd. and use thereof)
- IT 37318-49-3, Protein disulfide isomerase
(substantially cell membrane-impermeable compd. and use thereof)
- L99 ANSWER 14 OF 28 HCA COPYRIGHT 2004 ACS on STN
- 134:141330 Identification of the human liver cytochrome P450 isoenzyme responsible for the 6-methylhydroxylation of the novel anticancer drug 5,6-dimethylxanthenone-4-acetic acid. Zhou, Shufeng; Paxton, James W.; Tingle, Malcolm D.; Kestell, Philip (Department of Pharmacology and Clinical Pharmacology, The University of Auckland, Auckland, N. Z.). Drug Metabolism and Disposition, 28(12), 1449-1456 (English) 2000. CODEN: DMDSAI. ISSN: 0090-9556. Publisher: American Society for Pharmacology and Experimental Therapeutics.
- AB In vitro studies were conducted to identify the hepatic cytochrome P 450 (CYP) isoenzyme involved in the 6-methylhydroxylation of 5,6-dimethylxanthenone-4-acetic acid (DMXAA) by using a human liver library (n = 14). The metabolite 6-hydroxymethyl-5-methylxanthenone-4-acetic acid (6-OH-MXAA) was detd. by HPLC with fluorescence detection. The metabolite formed in human liver microsomes and by cDNA-expressed CYP isoform was identified by liq. chromatog. mass spectrometry as 6-OH-MXAA. In human liver microsomes (n = 14), 6-methylhydroxylation of DMXAA followed monophasic Michaelis-Menten kinetics, with a mean apparent Km of 21

.+-. 5 .mu.M and Vmax of 0.043 .+-. 0.019 nmol/min/mg. An approx. 10-fold interindividual variation in the intrinsic clearance (Vmax/Km) of DMXAA 6-methylhydroxylation in human liver microsomes was obsd. The involvement of CYP1A2 in DMXAA metab. by human livers was demonstrated by the following: 1) the potent inhibition of DMXAA metab. by furafylline (kinact = 0.23 .+-. 0.04 min⁻¹, K'app = 15.6 .+-. 6.7 .mu.M) and .alpha.-naphthoflavone (Ki = 0.036 .mu.M), but not by cimetidine, ketoconazole, tolbutamide, quinidine, chlorzoxazone, diethyldithiocarbamate, troleandomycin, and sulfaphenazole; 2) when incubated with human lymphoblastoid cell microsomes contg. cDNA-expressed CYP isoenzymes, DMXAA was metabolized only by CYP1A2, with an apparent Km of 6.2 .+-. 1.5 .mu.M and Vmax of 0.014 .+-. 0.001 nmol/min/mg, but not by CYP2A6, CYP2B6, CYP2C9 (Arg144), CYP2C19, CYP2D6 (Val374), CYP2E1, and CYP3A4; 3) a significant correlation (r = 0.90; P < .001) between 6-methylhydroxylation of DMXAA and 7-ethoxyresorufin O-deethylation; and 4) a significant correlation (r = 0.75; P < .01) between the CYP1A protein level detd. by Western blots and DMXAA 6-methylhydroxylation.

IT 117570-53-3, 5,6-Dimethylxanthene-4-acetic acid
(human liver cytochrome P 450 isoenzyme responsible for
methylhydroxylation of dimethylxantheneacetic acid)
RN 117570-53-3 HCA
CN 9H-Xanthene-4-acetic acid, 5,6-dimethyl-9-oxo- (9CI) (CA INDEX
NAME)



IT 223261-32-3
(human liver cytochrome P 450 isoenzyme responsible for
methylhydroxylation of dimethylxantheneacetic acid)
RN 223261-32-3 HCA
CN 9H-Xanthene-4-acetic acid, 6-(hydroxymethyl)-5-methyl-9-oxo- (9CI)
(CA INDEX NAME)



CC 1-2 (Pharmacology)

IT 117570-53-3, 5,6-Dimethylxanthenone-4-acetic acid
(human liver cytochrome P 450 isoenzyme responsible for
methylhydroxylation of dimethylxanthenoneacetic acid)

IT 223261-32-3
(human liver cytochrome P 450 isoenzyme responsible for
methylhydroxylation of dimethylxanthenoneacetic acid)

L99 ANSWER 15 OF 28 HCA COPYRIGHT 2004 ACS on STN

134:27295 Methods for producing 5'-nucleic acid-**protein**
conjugates. Lohse, Peter; Wright, Martin C.; McPherson, Michael
(Phylos, Inc., USA). PCT Int. Appl. WO 2000072869 A1 20001207, 32
pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG,
BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO,
RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU,
ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF,
CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC,
ML, MR, NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2.
APPLICATION: WO 2000-US15077 20000601. PRIORITY: US 1999-PV137032
19990601.

AB Disclosed herein is a method for generating a 5'-nucleic acid-
protein conjugate, the method involving: (a) providing a
nucleic acid which carries a reactive group at its 5'end; (b)
providing a non-derivatized **protein**; and (c) contacting
the nucleic acid and the **protein** under conditions which
allow the reactive group to react with the N-terminus of the
protein, thereby forming a 5'-nucleic acid-**protein**
conjugate. In one approach, fusions are formed by reaction between
an unprotected **protein** carrying an N-terminal
cysteine and a nucleic acid carrying a 1,2-aminothiol
reactive group. In a second approach, fusion formation occurs as
the result of a biarsenical-**tetracysteine** interaction.
Also disclosed herein are 5'-nucleic acid-**protein**
conjugates and methods for their use in (1) the selection of a
desired nucleic acid or a desired **protein** by sepg. the

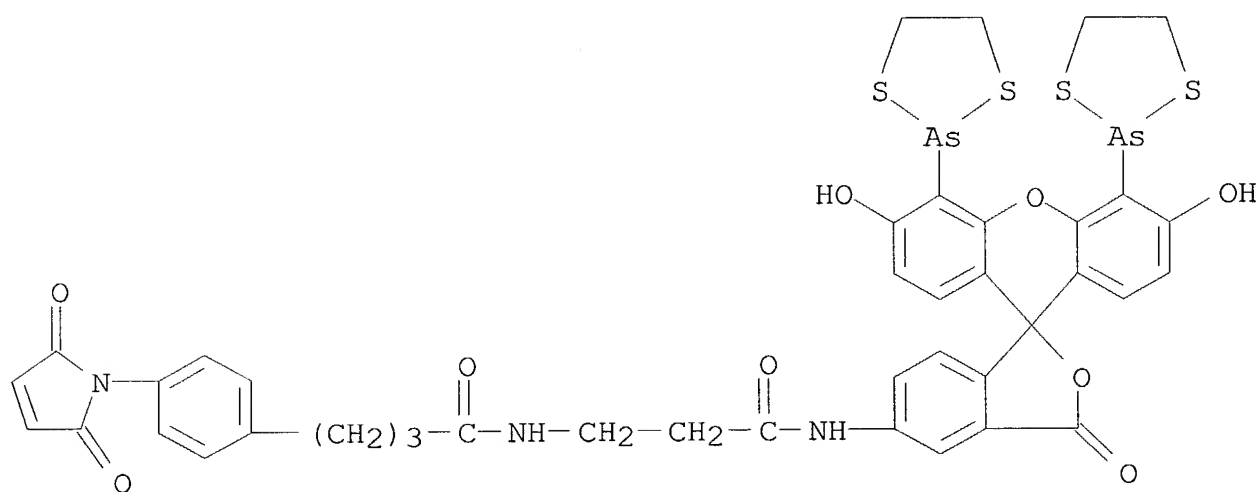
binding partner-candidate conjugate complex from unbound members of a population, and (2) detecting an interaction between a **protein** and a compd.

IT 311797-39-4P

(methods for producing 5'-nucleic acid-**protein** conjugates)

RN 311797-39-4 HCA

CN Benzenebutanamide, N-[3-[[4',5'-bis(1,3,2-dithiarsolan-2-yl)-3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl]amino]-3-oxopropyl]-4-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)- (9CI) (CA INDEX NAME)



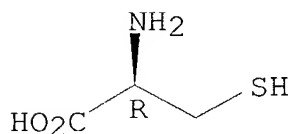
IT 52-90-4, L-Cysteine, reactions

(reaction with nucleic acid carrying a 1,2-aminothiol reactive group; methods for producing 5'-nucleic acid-**protein** conjugates)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IC ICM A61K038-16

ICS A61K038-03; C07K014-00

CC 9-16 (Biochemical Methods)

Section cross-reference(s): 33, 34

- ST nucleic acid conjugate **protein**
- IT Thiols (organic), reactions
(amino, nucleic acids contg., reaction with N-terminal cysteinyl
proteins; methods for producing 5'-nucleic acid-
protein conjugates)
- IT DNA
Nucleic acids
Proteins, specific or class
RNA
mRNA
(conjugates; methods for producing 5'-nucleic acid-
protein conjugates)
- IT **Nucleoproteins**
(methods for producing 5'-nucleic acid-**protein**
conjugates)
- IT Amines, reactions
(thiol, nucleic acids contg., reaction with N-terminal cysteinyl
proteins; methods for producing 5'-nucleic acid-
protein conjugates)
- IT 56377-57-2
(methods for producing 5'-nucleic acid-**protein**
conjugates)
- IT 311797-38-3P **311797-39-4P**
(methods for producing 5'-nucleic acid-**protein**
conjugates)
- IT **52-90-4, L-Cysteine**, reactions
(reaction with nucleic acid carrying a 1,2-aminothiol reactive
group; methods for producing 5'-nucleic acid-**protein**
conjugates)
- IT 312323-65-2 312323-66-3 312323-67-4 312343-85-4
(unclaimed sequence; methods for producing 5'-nucleic acid-
protein conjugates)

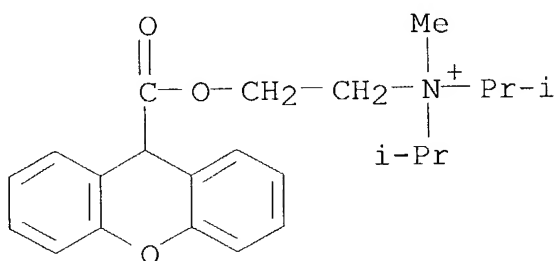
L99 ANSWER 16 OF 28 HCA COPYRIGHT 2004 ACS on STN

134:500 Method for activity profiling compound mixtures. Pidgeon,
Charles; Rooke, Nadege M.; Ruell, Jeffrey A. (Admetric Biochem Inc.,
USA). PCT Int. Appl. WO 2000070344 A2 20001123, 84 pp. DESIGNATED
STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH,
CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ,
BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM,
CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL,
PT, SE, SN, TD, TG. (English). CODEN: PIXXD2. APPLICATION: WO
2000-US13178 20000512. PRIORITY: US 1999-PV133968 19990513.

AB A method is described for identifying compds. in a complex mixt.
exhibiting a predetd. characteristic. The mixt. is sepd. into

fractions using at least two unique sets of sepn. parameters to produce at least two series of sepn. parameter dependent fractions. In one embodiment the mixts. are sepd. chromatog. using unique sets of sepn. parameters and the fractions are analyzed spectroscopically to provided data indicative of the component compds. and the fractions are either analyzed individually, or in synchronously combined fractions, for the predetd. characteristic. The spectroscopic data for the fractions exhibiting the predetd. characteristic are compared to identify compd.(s) common to the fractions exhibiting the characteristic. The method can be implemented in an automatic chromatog. system to provide rapid screening of complex compd. mixts. for predetd. chem. or biol. characteristics and to identify those components of the mixt. exhibiting such characteristics. The invention can be applied to the rapid and efficient collection of databases of chromatog. fingerprints for large compd. libraries and seems perfectly suited for lead identification and optimization of chem. libraries, which is a very important aspect of the drug discovery process, as well as QSAR studies.

IT 298-50-0, Propantheline
 (activity profiling of compd. mixts.)
 RN 298-50-0 HCA
 CN 2-Propanaminium, N-methyl-N-(1-methylethyl)-N-[2-[(9H-xanthen-9-ylcarbonyl)oxy]ethyl]- (9CI) (CA INDEX NAME)



IC ICM G01N033-53
 CC 1-1 (Pharmacology)
 Section cross-reference(s): 9
 IT **Mass spectrometry**
 (HPLC combined with; activity profiling of compd. mixts.)
 IT Chromatography
 Combinatorial library
 Drug screening
 HPLC
 IR spectroscopy
Mass spectrometry
 NMR spectroscopy
 Separation

- Spectroscopy
 Toxicity
 UV and visible spectroscopy
 (activity profiling of compd. mixts.)
- IT Natural products
 Protein hydrolyzates
Proteins, general, analysis
 (activity profiling of compd. mixts.)
- IT HPLC
 (mass spectrometry combined with; activity
 profiling of compd. mixts.)
- IT 50-49-7, Imipramine 51-55-8, Atropine, analysis 52-86-8,
 Haloperidol 54-04-6, Mescaline 54-05-7, Chloroquine 54-30-8,
 Camylofin 58-25-3, Chlordiazepoxide 58-73-1, Diphenhydramine
 59-26-7, Nikethamide 59-32-5, Chloropyramine 59-98-3, Tolazoline
 64-95-9, Adiphenine 68-88-2, Hydroxyzine 77-23-6, Carbetapentane
 77-37-2, Procyclidine 82-92-8, Cyclizine 83-98-7, Orphenadrine
 86-22-6, Brompheniramine 91-75-8, Antazoline 91-80-5,
 Methapyrilene 92-12-6, Phenyltoloxamine 93-30-1,
 Methoxyphenamine 99-43-4, Benoxinate 125-53-1, Oxyphencyclimine
 130-95-0, Quinine 132-22-9, Chlorpheniramine 144-11-6
298-50-0, Propantheline 299-42-3, Ephedrine 439-14-5,
 Diazepam 486-47-5, Ethaverine 512-15-2, Cyclopentolate
 586-60-7, Dyclonine 636-54-4, Clopamide 642-72-8, Benzydamine
 1491-59-4, Oxymetazoline 1508-75-4, Tropicamide 1668-19-5,
 Doxepin 1977-10-2, Loxapine 2086-83-1, Berberine 2898-12-6,
 Medazepam 2955-38-6, Prazepam 3820-67-5, Glafenine 5053-06-5,
 Fenspiride 5633-20-5, Oxybutynin 5845-26-1, Thiazesim
 12794-10-4D, Benzodiazepine, derivs. 13392-18-2, Fenoterol
 13655-52-2, Alprenolol 14051-33-3, Benzetimide 14214-84-7,
 Oxyphenonium 17617-23-1, Flurazepam 18559-94-9, Salbutamol
 21888-98-2, Dexetimide 23256-50-0, Guanabenz acetate 24219-97-4,
 Mianserin 26839-75-8, Timolol 30516-87-1, AZT 34368-04-2,
 Dobutamine 36894-69-6, Labetalol 37148-27-9, Clenbuterol
 37517-30-9, Acebutolol 40796-97-2 41094-88-6, Tracazolate
 42399-41-7, Diltiazem 50679-08-8, Terfenadine 51264-14-3,
 Amsacrine 54063-53-5, Propafenone 54143-55-4, Flecainide
 57149-07-2, Naftopidil 60205-81-4, Ipratropium 65277-42-1,
 Ketoconazole 70458-96-7, Norfloxacin 82626-48-0, Zolpidem
 84371-65-3, Mifepristone
 (activity profiling of compd. mixts.)

L99 ANSWER 17 OF 28 HCA COPYRIGHT 2004 ACS on STN

133:361699 A diverse set of oligomeric class II MHC-peptide
 complexes for probing T-cell receptor interactions. Cochran,
 Jennifer R.; Stern, Lawrence J. (Department of Chemistry,
 Massachusetts Institute of Technology, Cambridge, MA, 02139, USA).
 Chemistry & Biology, 7(9), 683-696 (English) 2000. CODEN: CBOLE2.

ISSN: 1074-5521. Publisher: Elsevier Science Ltd..

AB Background: T-cells are activated by engagement of their clonotypic cell surface receptors with **peptide** complexes of major histocompatibility complex (MHC) **proteins**, in a poorly understood process that involves receptor clustering on the membrane surface. Few tools are available to study the mol. mechanisms responsible for initiation of activation processes in T-cells. Results: A topol. diverse set of oligomers of the human MHC **protein** HLA-DR1, varying in size from dimers to tetramers, was produced by varying the location of an introduced **cysteine** residue and the no. and spacing of sulfhydryl-reactive groups carried on novel and com. available crosslinking reagents. Fluorescent probes incorporated into the crosslinking reagents facilitated measurement of oligomer binding to the T-cell surface. Oligomeric MHC-**peptide** complexes, including a variety of MHC dimers, trimers and tetramers, bound to T-cells and initiated T-cell activation processes in an antigen-specific manner. Conclusion: T-cell receptor dimerization on the cell surface is sufficient to initiate intracellular signaling processes, as a variety of MHC-**peptide** dimers differing in intramol. spacing and orientation were each able to trigger early T-cell activation events. The relative binding affinities within a homologous series of MHC-**peptide** oligomers suggest that T-cell receptors may rearrange in the plane of the membrane concurrent with oligomer binding.

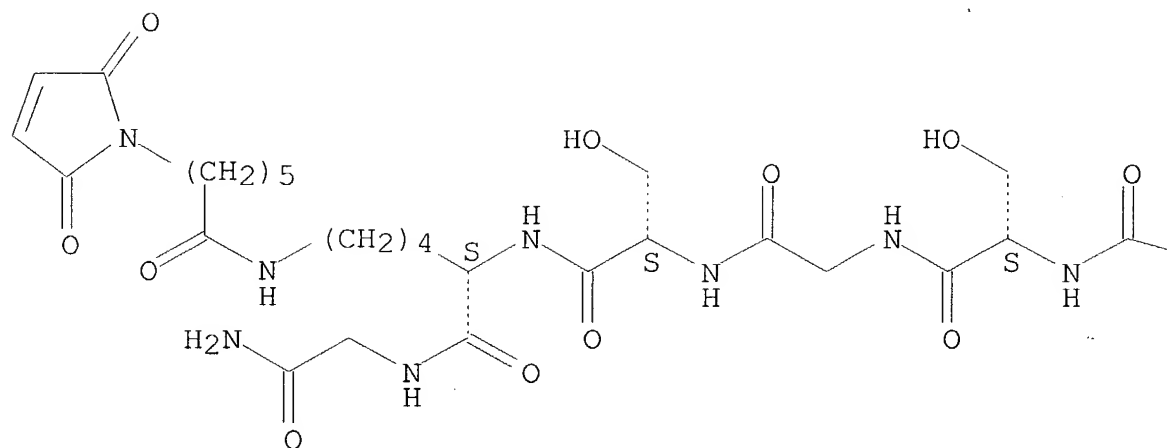
IT 272788-73-5 272789-77-2
(for prepn. of oligomeric class II MHC-**peptide** complexes)

RN 272788-73-5 HCA

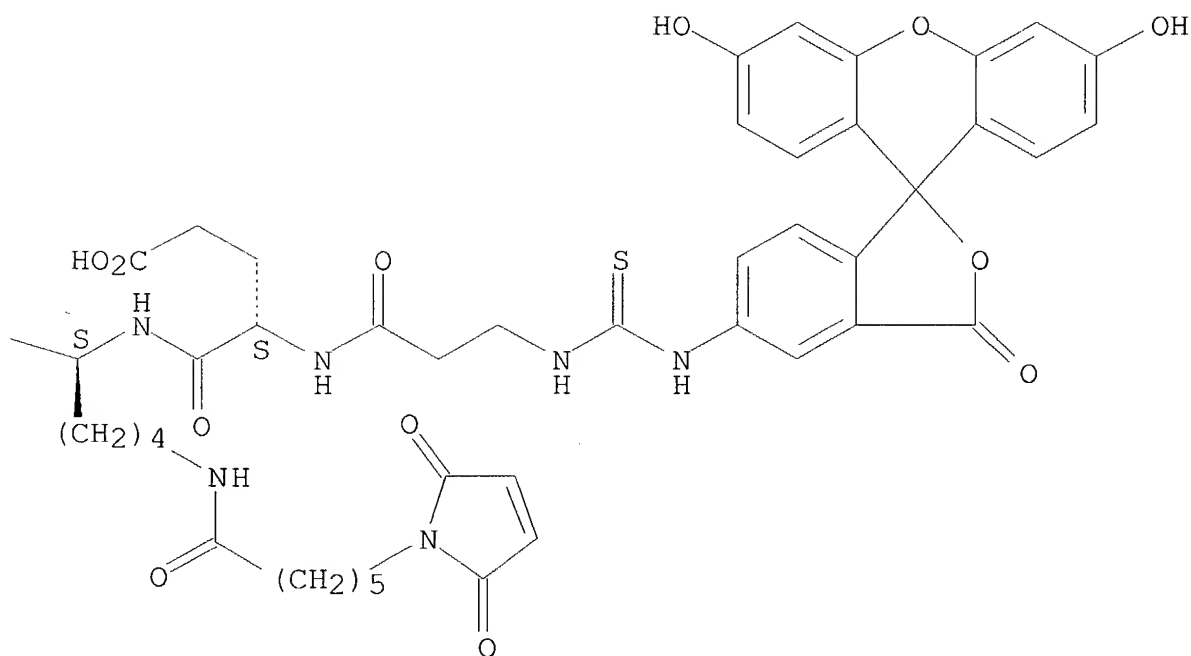
CN Glycinamide, N-[[[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)amino]thioxomethyl]-.beta.-alanyl-L-.alpha.-glutamyl-N6-[6-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)-1-oxohexyl]-L-lysyl-L-seryl]glycyl-L-seryl-N6-[6-(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)-1-oxohexyl]-L-lysyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



PAGE 1-B

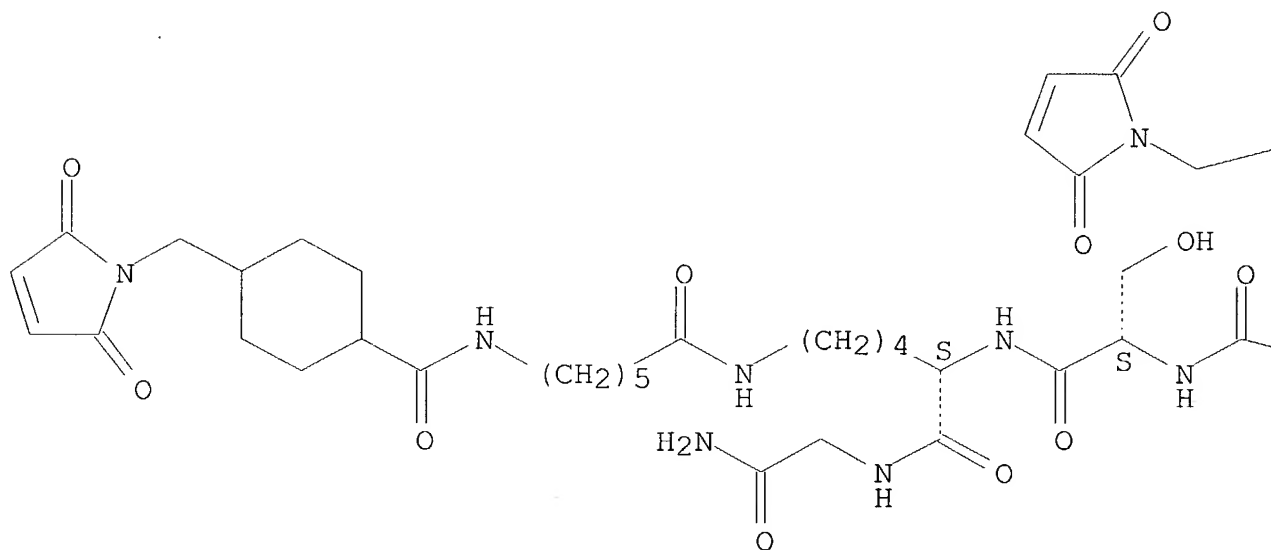


RN 272789-77-2 HCA
CN Glycinamide, N-[[[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9']-

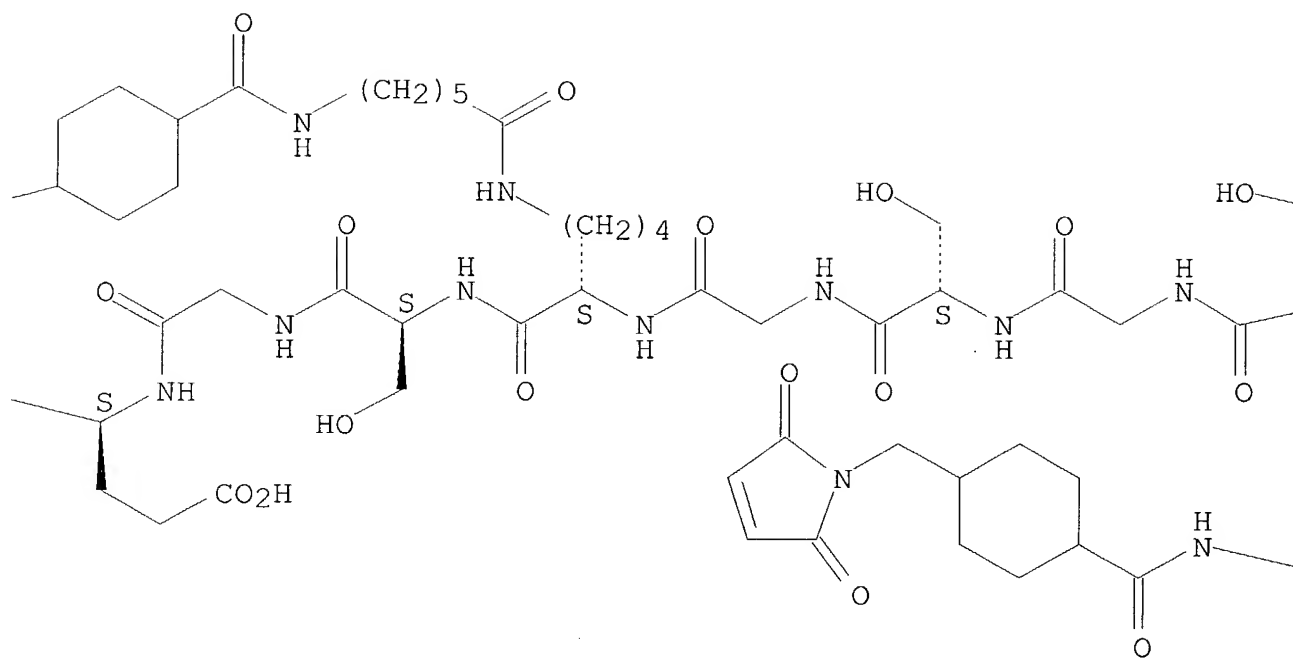
[9H]xanthen]-5-yl)amino]thioxomethyl]-.beta.-alanyl-L-.alpha.-glutamyl-N6-[6-[[[4-[(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)methyl]cyclohexyl]carbonyl]amino]-1-oxohexyl]-L-lysyl-L-serylglycyl-L-serylglycyl-N6-[6-[[[4-[(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)methyl]cyclohexyl]carbonyl]amino]-1-oxohexyl]-L-lysyl-L-serylglycyl-L-.alpha.-glutamyl-L-seryl-N6-[6-[[[4-[(2,5-dihydro-2,5-dioxo-1H-pyrrol-1-yl)methyl]cyclohexyl]carbonyl]amino]-1-oxohexyl]-L-lysyl- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A

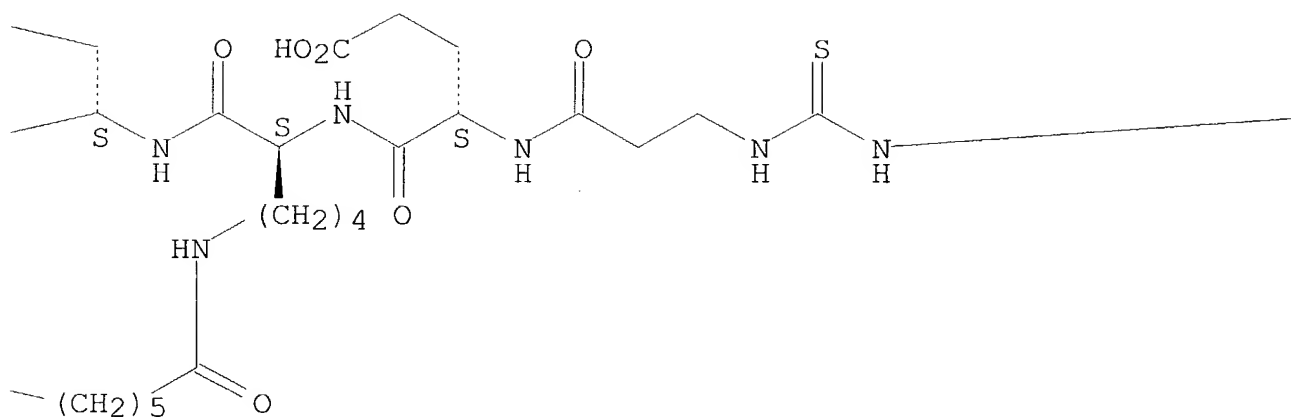


PAGE 1-B

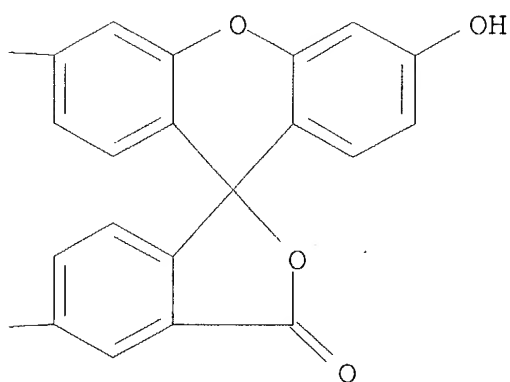


PAGE 1-C

HO—



PAGE 1-D



CC 15-1 (Immunochemistry)
 ST oligomer MHC **peptide** complex T cell activation; TCR
 receptor interaction oligomer MHC **peptide** complex
 IT TCR .alpha..beta. (receptor)
 TCR .alpha..beta. (receptor)
 (CD3 complex; oligomeric class II MHC-**peptide** complexes
 for probing T-cell activation via)

- IT Histocompatibility antigens
(HLA-DR1, complexes, with antigenic **peptides**;
antigen-specific T-cell activation in response to oligomers of)
- IT Cell activation
(T cell; by oligomeric class II MHC-**peptide** complexes)
- IT CD3 (antigen)
CD3 (antigen)
(TCR .alpha..beta. complex; oligomeric class II MHC-
peptide complexes for probing T-cell activation via)
- IT T cell (lymphocyte)
(activation; by oligomeric class II MHC-**peptide**
complexes)
- IT **Peptides**, biological studies
(complexes, complexes, with HLA-DR1; antigen-specific T-cell
activation in response to oligomers of)
- IT 272788-73-5 272789-77-2 272789-78-3
(for prepn. of oligomeric class II MHC-**peptide**
complexes)

L99 ANSWER 18 OF 28 HCA COPYRIGHT 2004 ACS on STN

133:172215 Controlling **protein** levels in eucaryotic organisms
using novel compds. comprising a ubiquitination recognition element
and a **protein** binding element. Kenten, John H.; Roberts,
Steven F.; Lebowitz, Michael S. (Proteinix, Inc., USA). PCT Int.
Appl. WO 2000047220 A1 20000817, 106 pp. DESIGNATED STATES: W: AE,
AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK,
EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG,
KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO,
NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG,
US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT,
BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR,
IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG. (English).
CODEN: PIXXD2. APPLICATION: WO 2000-US3436 20000211. PRIORITY: US
1999-PV119851 19990212; US 1999-406781 19990928.

AB The invention relates to novel compds. comprising a ubiquitination
recognition element and a **protein** binding element. The
invention also relates to the use of said compds. for modulating the
level and/or activity of a target **protein**. The compds.
are useful for the treatment of diseases such as infections,
inflammatory conditions, cancer and genetic diseases. The compds.
are also useful as insecticides and herbicides.

IT 288257-29-4
(fluorescein antibodies targeted degrdn. stimulation by;
controlling **protein** levels in eucaryotic organisms
using novel compds. comprising a ubiquitination recognition
element and a **protein** binding element and use as drugs
and pesticides)

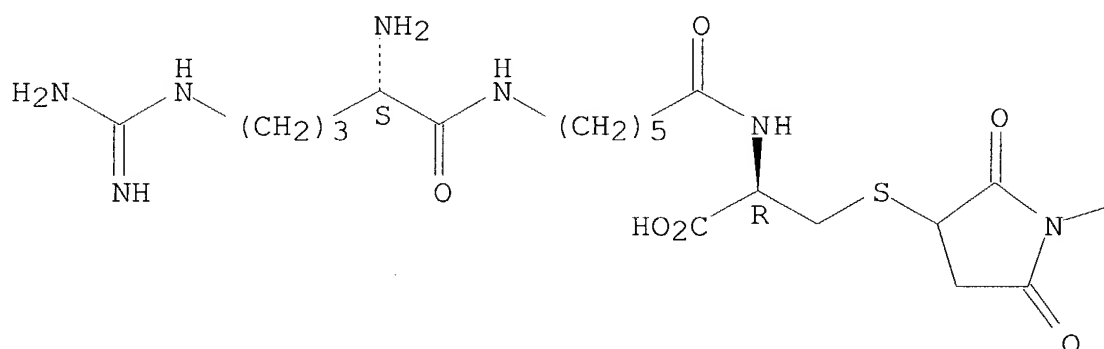
RN 288257-29-4 HCA

CN L-Cysteine, L-arginyl-6-aminohexanoyl-S-[1-(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)-2,5-dioxo-3-pyrrolidinyl]- (9CI) (CA INDEX NAME)

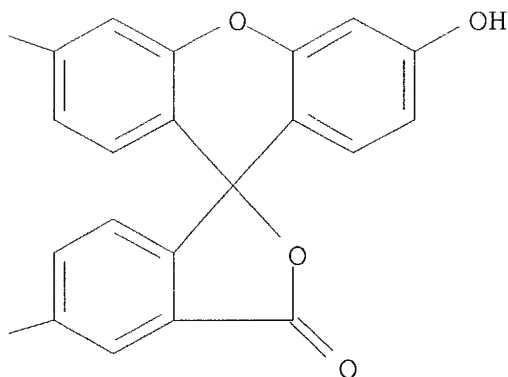
Absolute stereochemistry.

PAGE 1-A

HO—



PAGE 1-B



IC ICM A61K038-00
 CC 1-12 (Pharmacology)
 Section cross-reference(s): 5
 ST **protein** control ubiquitination **recognition**
 element; pharmacol **protein** control ubiquitination
recognition element; pesticide **protein** control

- ubiquitination **recognition** element; insecticide
protein control ubiquitination **recognition**
element; herbicide **protein** control ubiquitination
recognition element
- IT **Protein** motifs
(Deg1, ubiquitination recognition element binding to; controlling
protein levels in eucaryotic organisms using novel
compds. comprising a ubiquitination recognition element and a
protein binding element)
- IT **Protein** motifs
(Deg2, ubiquitination recognition element binding to; controlling
protein levels in eucaryotic organisms using novel
compds. comprising a ubiquitination recognition element and a
protein binding element)
- IT Histocompatibility antigens
(MHC (major histocompatibility complex), class I, targeted
degrdn. of; controlling **protein** levels in eucaryotic
organisms using novel compds. comprising a ubiquitination
recognition element and a **protein** binding element and
use as drugs and pesticides)
- IT Histocompatibility antigens
(MHC (major histocompatibility complex), class II, targeted
degrdn. of; controlling **protein** levels in eucaryotic
organisms using novel compds. comprising a ubiquitination
recognition element and a **protein** binding element and
use as drugs and pesticides)
- IT Histocompatibility antigens
(MHC (major histocompatibility complex), targeted degrdn. of;
controlling **protein** levels in eucaryotic organisms
using novel compds. comprising a ubiquitination recognition
element and a **protein** binding element and use as drugs
and pesticides)
- IT **Protein** motifs
(N-end N-recognin, ubiquitination recognition element binding to;
controlling **protein** levels in eucaryotic organisms
using novel compds. comprising a ubiquitination recognition
element and a **protein** binding element)
- IT **Protein** motifs
(PEST motif, ubiquitination recognition element binding to;
controlling **protein** levels in eucaryotic organisms
using novel compds. comprising a ubiquitination recognition
element and a **protein** binding element)
- IT **Protein** motifs
(WW domain, ubiquitination recognition element binding to;
controlling **protein** levels in eucaryotic organisms
using novel compds. comprising a ubiquitination recognition
element and a **protein** binding element)
- IT Anti-AIDS agents

- Anti-infective agents
- Antitumor agents
- Antiviral agents
- Parasitocides
- Pesticides
- Protein degradation**
(controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT **Peptides**, biological studies
(controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT **Proteins**, general, biological studies
(controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT **Protein motifs**
(delta domain, ubiquitination recognition element binding to; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element)
- IT **Protein motifs**
(destruction box, ubiquitination recognition element binding to; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element)
- IT **Protein motifs**
(phosphorylated sequences, ubiquitination recognition element binding to; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element)
- IT **Antigens**
Thioredoxins
(targeted degrdn. of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT **Antibodies**
(to fluorescein, targeted degrdn. of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT **Cytomegalovirus**
Hepatitis A virus

- Hepatitis B virus
 Hepatitis C virus
 Hepatitis GB virus C/G
 Human herpesvirus
 Human immunodeficiency virus 1
 Human immunodeficiency virus 2
 Rabies virus
 Rous sarcoma virus
 (treatment of infection with; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT Enzymes, biological studies
 (ubiquitin-conjugating; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT Hepatitis
 (viral, treatment of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 288257-27-2
 (HIV integrase targeted degrdn. stimulation by; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 52350-85-3, Integrase
 (HIV, targeted degrdn. of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 2321-07-5, Fluorescein
 (antibodies to, targeted degrdn. of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 28971-77-9D, linker derivs. 112558-12-0D, linker derivs.
 288256-96-2 288256-97-3 288256-98-4 288256-99-5 288257-00-1
 288257-01-2 288257-02-3 288257-03-4 288257-04-5 288257-05-6
 288257-06-7 288257-07-8 288257-08-9D, linker derivs.
 288257-09-0D, linker derivs. 288257-10-3D, linker derivs.
 288257-11-4D, linker derivs. 288257-12-5D, linker derivs.
 288257-13-6D, linker derivs. 288257-14-7D, linker derivs.
 288257-15-8D, linker derivs. 288257-16-9D, linker derivs.
 288257-17-0D, linker derivs. 288257-18-1 288257-19-2
 288257-20-5 288257-21-6 288257-22-7 288257-23-8 288257-24-9
 (as ubiquitination **recognition** element; controlling

- protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 60267-61-0, Ubiquitin 74812-49-0, E3 Ubiquitin ligase
(controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 288257-29-4
(fluorescein antibodies targeted degrdn. stimulation by; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 288257-28-3
(glutathione S-transferase targeted degrdn. stimulation by; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 288257-25-0
(lysozyme targeted degrdn. stimulation by; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 288257-26-1
(streptavidin targeted degrdn. stimulation by; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 50812-37-8, Glutathione S-transferase
(targeted degrdn. of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 9001-63-2, Lysozyme
(targeted ubiquitination and degrdn. of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 9013-20-1, Streptavidin
(targeted ubiquitination of; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element and use as drugs and pesticides)
- IT 288387-73-5
(unclaimed **protein** sequence; controlling **protein** levels in eucaryotic organisms using novel

compds. comprising a ubiquitination recognition element and a **protein** binding element)

IT	124676-51-3	124676-52-4	124676-53-5	191606-36-7	223673-79-8
	246863-05-8	248909-28-6	248909-79-7	248909-90-2	250255-96-0
	252032-31-8	268741-28-2	288315-45-7	288315-49-1	288315-54-8
	288315-59-3	288315-61-7	288315-63-9	288315-65-1	288315-67-3
	288315-69-5	288315-71-9	288315-73-1	288315-75-3	288315-77-5
	288315-79-7	288315-82-2	288315-85-5	288315-87-7	288315-89-9
	288315-91-3	288315-93-5	288315-95-7	288315-97-9	288315-99-1
	288316-01-8	288316-03-0	288316-05-2	288316-07-4	288316-10-9
	288316-12-1	288316-14-3	288316-16-5	288387-74-6	

(unclaimed sequence; controlling **protein** levels in eucaryotic organisms using novel compds. comprising a ubiquitination recognition element and a **protein** binding element)

L99 ANSWER 19 OF 28 HCA COPYRIGHT 2004 ACS on STN

131:141745 Energy transfer dyes as labels in biological systems. Flick, Parke (Amersham Pharmacia Biotech, Inc., USA). PCT Int. Appl. WO 9939203 A1 19990805, 31 pp. DESIGNATED STATES: W: AU, CA, JP; RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1999-US2105 19990202. PRIORITY: US 1998-18111 19980203.

AB A novel class of energy transfer dyes, their prepn., and their use as labels in biol. systems is disclosed. The dyes are preferably in the form of cassettes which enable their attachment to a variety of biol. materials. The dyes and the reagents that can be made from them offer a wide variety of fluorescent labels with large Stokes' shifts enabling their use in a variety of fluorescence applications over a wide range of the visible spectrum. Prepn. of FAM-**Cysteine**-linker-ROX energy transfer dye from L-**cysteine**, 5-iodoacetamidofluorescein, trifluoroacetyl-protected NHS ester of 6-aminocaproic acid and 5'-ROX-NHS ester is described. With excitation at 488 nm, a strong peak was obsd. at 603 nm, characteristic of the ROX emission and indicating excellent energy transfer.

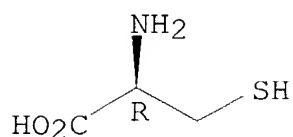
IT 52-90-4, L-**Cysteine**, reactions

(in prepn. of energy transfer dye; energy transfer dyes as labels in biol. systems)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



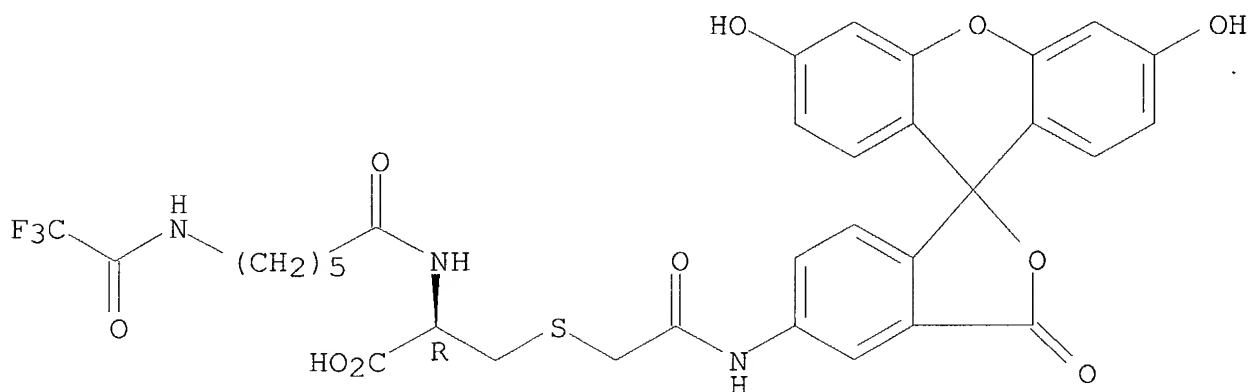
IT 235749-12-9P

(in prepn. of energy transfer dye; energy transfer dyes as labels in biol. systems)

RN 235749-12-9 HCA

CN L-Cysteine, S-[2-[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)amino]-2-oxoethyl]-N-[1-oxo-6-[(trifluoroacetyl)amino]hexyl]- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IC ICM G01N033-533

ICS C07D311-82; C07D311-88; C07K016-00; C12N009-96; G01N033-52; G01N033-533; G01N033-545; G01N033-548; G01N033-552; G01N033-554

CC 9-14 (Biochemical Methods)

Section cross-reference(s): 41

IT Antibodies

Enzymes, uses

Lipids, uses

Nucleic acids

Peptides, uses

Proteins, specific or class

(conjugates, with dyes; energy transfer dyes as labels in biol. systems)

IT Antibodies

Antigens

Carbohydrates, reactions

DNA

Lipids, reactions

Nucleotides, reactions

Peptides, reactions

Proteins, general, reactions

RNA

(fluorescent labeling of; energy transfer dyes as labels in biol. systems)

IT 52-90-4, L-Cysteine, reactions 63368-54-7,
5-Iodoacetamidofluorescein 117032-51-6 209734-74-7
(in prepn. of energy transfer dye; energy transfer dyes as labels
in biol. systems)

IT 235749-11-8P 235749-12-9P
(in prepn. of energy transfer dye; energy transfer dyes as labels
in biol. systems)

L99 ANSWER 20 OF 28 HCA COPYRIGHT 2004 ACS on STN

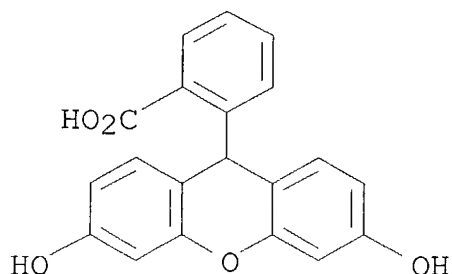
131:29566 Devices and methods for detecting target molecules in
biological samples. Muir, Andrew R.; Boles, Truett C.; Adams,
Christopher P. (Mosaic Technologies, USA). PCT Int. Appl. WO
9926724 A2 19990603, 124 pp. DESIGNATED STATES: W: AL, AM, AT, AU,
AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB,
GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK,
LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW,
AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH,
CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR,
NE, NL, PT, SE, SN, TD, TG. (English). CODEN: PIXXD2.
APPLICATION: WO 1998-US24918 19981125. PRIORITY: US 1997-66508
19971125.

AB Devices and methods for detecting the presence, or absence of the
presence, of at least one target mol. employing a receptacle housing
a reaction chamber comprised of at least one compartment contg.
suitable reagents for the detection of the target mol. are
disclosed. The device can be used in particular for screening
donated blood or other biol. fluids for the presence of
contaminants. Preferably, the device comprises two or more
breakable compartments sepd. by breakable barriers, and is assocd.
with a collection system such as a blood bag. Probes and assays for
detection of eubacterial contamination in platelet conc. are
described.

IT 518-44-5, Fluorescein
(donor probe labeled with, for detection of eubacterial 16S rRNA
in platelet conc.; devices and methods for detecting target mols.
in biol. samples)

RN 518-44-5 HCA

CN Benzoic acid, 2-(3,6-dihydroxy-9H-xanthen-9-yl)- (9CI) (CA INDEX
NAME)



- IC ICM B01L003-00
ICS G01N033-49; C12Q001-68; A61M001-02
- CC 9-1 (Biochemical Methods)
Section cross-reference(s): 3, 10, 63
- IT Chromophores
Fluorescent substances
Luminescent substances
Radioactive substances
(as **probe** label; devices and methods for detecting target mols. in biol. samples)
- IT DNA
Nucleic acids
Peptides, analysis
Polynucleotides
Proteins, general, **analysis**
RNA
(as target; devices and methods for detecting target mols. in biol. samples)
- IT Antibodies
(labeled, compartment contg., for **detecting proteins**; devices and methods for detecting target mols. in biol. samples)
- IT **518-44-5**, Fluorescein
(donor probe labeled with, for detection of eubacterial 16S rRNA in platelet conc.; devices and methods for detecting target mols. in biol. samples)
- L99 ANSWER 21 OF 28 HCA COPYRIGHT 2004 ACS on STN
128:190109 A Homobifunctional Rhodamine for Labeling **Proteins** with Defined Orientations of a Fluorophore. Corrie, John E. T.; Craik, James S.; Munasinghe, V. Ranjit N. (National Institute for Medical Research, London, NW7 1AA, UK). Bioconjugate Chemistry, 9(2), 160-167 (English) 1998. CODEN: BCCHEs. ISSN: 1043-1802. Publisher: American Chemical Society.
- AB The synthesis and characterization of a bifunctional rhodamine dye bearing 2-(iodoacetamido)ethyl substituents on the 3'- and 6'-nitrogen atoms is described. Aspects of the conversion of chloroacetamides to iodoacetamides are discussed, including a

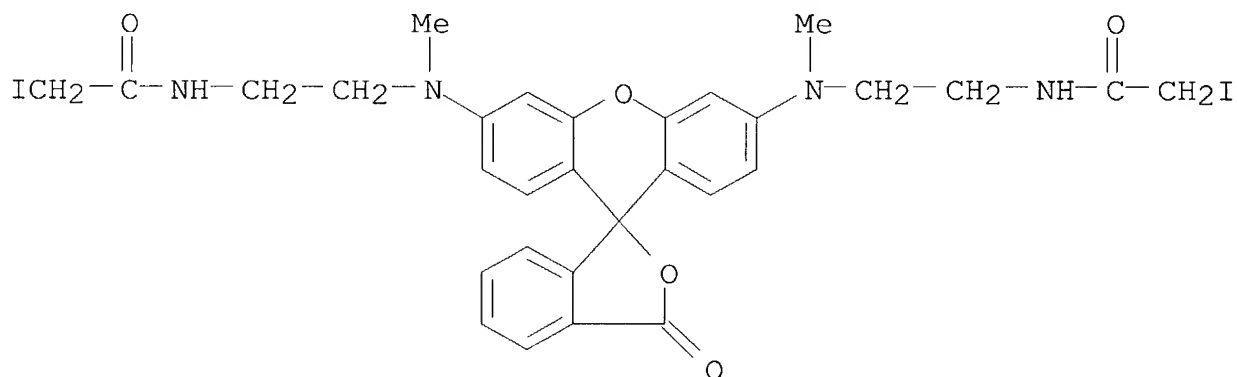
remarkably mild dehalogenation of an arom. haloacetamide in the presence of NaI and camphorsulfonic acid. The bifunctional rhodamine was designed for 2-site, 1:1 labeling of **proteins** that contain 2 suitably disposed **cysteine** residues and is intended to constrain the orientation of the rhodamine absorption and emission dipoles in a predictable relationship to the **protein** structure.

IT 203580-70-5P

(prepn. of homobifunctional rhodamine for labeling **proteins**)

RN 203580-70-5 HCA

CN Acetamide, N,N'-[(3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthene]-3',6'-diyl)bis[(methylimino)-2,1-ethanediyl]]bis[2-iodo- (9CI) (CA INDEX NAME)

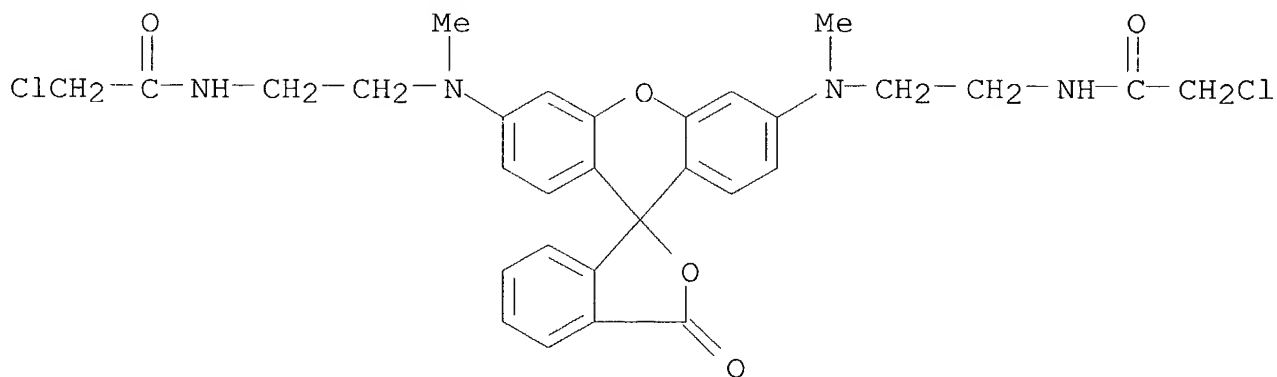


IT 203580-79-4P

(prepn. of homobifunctional rhodamine for labeling **proteins**)

RN 203580-79-4 HCA

CN Acetamide, N,N'-[(3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthene]-3',6'-diyl)bis[(methylimino)-2,1-ethanediyl]]bis[2-chloro- (9CI) (CA INDEX NAME)



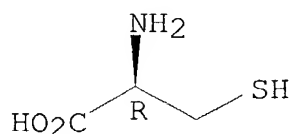
- CC 9-14 (Biochemical Methods)
Section cross-reference(s): 28, 41
- ST homobifunctional rhodamine labeling **protein** prepn
- IT **Proteins**, specific or class
(mercapto-contg.; prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT Fluorescent substances
(prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT Dehalogenation
Proteins, general, reactions
(prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT Myosins
(regulatory light-chain; prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT 203580-80-7
(prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT 203580-70-5P
(prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT 98-09-9, Benzenesulfonyl chloride 105-36-2, Ethyl bromoacetate
630-88-6 7452-78-0 26226-72-2
(prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT 14318-66-2P 33905-43-0P 116465-51-1P 203580-72-7P
203580-73-8P 203580-74-9P 203580-75-0P 203580-76-1P
203580-77-2P 203580-78-3P **203580-79-4P**
(prepn. of homobifunctional rhodamine for labeling **proteins**)
- IT 5338-44-3P 6080-04-2P 203580-69-2P
(prepn. of homobifunctional rhodamine for labeling **proteins**)
- L99 ANSWER 22 OF 28 HCA COPYRIGHT 2004 ACS on STN
127:288298 Irreversible Activation of the Gonadotropin-Releasing Hormone
Receptor by Photoaffinity Crosslinking: Localization of Attachment
Site to Cys Residue in N-Terminal Segment. Davidson, James S.;
Assefa, Daniel; Pawson, Adam; Davies, Peter; Hapgood, Janet; Becker,
Inga; Flanagan, Colleen; Roeske, Roger; Millar, Robert (M.R.C.
Regulatory Peptides Research Unit Department of Chemical Pathology,
University of Cape Town Medical School, Observatory, 7925, S. Afr.).
Biochemistry, 36(42), 12881-12889 (English) 1997. CODEN: BICHAW.
ISSN: 0006-2960. Publisher: American Chemical Society.
- AB Photoaffinity crosslinking with [azidobenzoyl-D-Lys6]GnRH leads to
irreversible activation of the gonadotropin-releasing hormone (GnRH)

receptor. In order to localize the crosslinking site, the **disulfide** bridge structure was initially probed by mutagenesis. A consistent pattern of changes in the ability of GnRH to stimulate signal transduction after Ser substitutions of extracellularly located Cys residues indicated that Cys14 in the N-terminal domain is connected to Cys200 in the second extracellular loop, while Cys196 in this loop is connected to the highly conserved Cys114 at the extracellular end of transmembrane helix 3.

Protein chem. anal. of radioactive fragments of cross-linked GnRH receptor following deglycosylation and enzymic **digest** with endoproteinase Glu-C and trypsin before and after introduction or elimination of potential protease cleavage sites indicated that ^{125}I [azidobenzoyl-D-Lys6]GnRH cross-links to a segment comprising residues 12-18 of the N-terminal domain. The existence of the Cys114-Cys196 bridge was directly confirmed as a labeled fragment, including that Cys114 was resolvable only under reducing conditions. The observation that the cross-linked N-terminal enzymic fragments had identical apparent size under non-reducing conditions shows that the crosslinking reaction disconnected the **disulfide** bridge between Cys14 and Cys200 and indicates that Cys14 is probably the residue involved in crosslinking of the ligand. It is concluded that covalent tethering of GnRH through a photoreactive side chain located at position 6 in the middle of the **peptide** leads to continued activation of the receptor presumably through covalent binding to Cys14 in the N-terminal domain of the receptor.

IT 52-90-4, L-Cysteine, biological studies
 (LH-RH receptor residue 14; LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
 RN 52-90-4 HCA
 CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



CC 2-2 (Mammalian Hormones)
 ST LHRH receptor photoaffinity crosslinking **disulfide** bridge
 IT **Disulfide** group
 Signal transduction, biological
 (LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
 IT Gonadotropin-releasing hormone receptor

- (LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
- IT Conformation
(loop, protein; LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
- IT Crosslinking
(photochem.; LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
- IT Helix (conformation)
(protein; LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
- IT 78527-81-8
(LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
- IT 9034-40-6, LH-RH
(LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
- IT 197100-47-3
(LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)
- IT 52-90-4, L-Cysteine, biological studies
(LH-RH receptor residue 14; LH-RH receptor irreversible activation by photoaffinity crosslinking with attachment to **cysteine** residue 14)

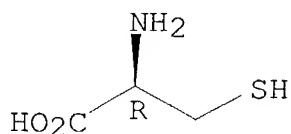
L99 ANSWER 23 OF 28 HCA COPYRIGHT 2004 ACS on STN

- 127:231138 Peptidylglycine .alpha.-hydroxylating monooxygenase: active site residues, **disulfide** linkages, and a two-domain model of the catalytic core. Kolhekar, Aparna S.; Keutmann, Henry T.; Mains, Richard E.; Quon, Andrew S. W.; Eipper, Betty A. (Johns Hopkins University School of Medicine, Baltimore, MD, 21205-2105, USA). Biochemistry, 36(36), 10901-10909 (English) 1997. CODEN: BICHAW. ISSN: 0006-2960. Publisher: American Chemical Society.
- AB Peptidylglycine .alpha.-hydroxylating monooxygenase (PHM) is a copper, ascorbate, and mol. oxygen dependent enzyme that catalyzes the first step leading to the C-terminal amidation of glycine-extended **peptides**. The catalytic core of PHM (PHMcc), refined to residues 42-356 of the PHM protein, was expressed at high levels in CHO (DG44) (dhfr-) cells. PHMcc has 10 **cysteine** residues involved in 5 **disulfide** linkages. Endoprotease Lys-C **digestion** of purified PHMcc under nonreducing conditions cleaved the **protein** at Lys219, **indicating** that the **protein** consists of separable N- and C-terminal domains with internal **disulfide** linkages, that are connected by an exposed linker region. **Disulfide**-linked **peptides** generated by sequential

CNBr and pepsin treatment of **radiolabeled** PHMcc were sepd. by reverse phase HPLC and identified by Edman degrdn. Three **disulfide** linkages occur in the N-terminal domain (Cys47-Cys186, Cys81-Cys126, and Cys114-Cys131), along with three of the His residues crit. to catalytic activity (His107, His108, and His172). Two **disulfide** linkages (Cys227-Cys334 and Cys293-Cys315) occur in the C-terminal domain, along with the remaining two essential His residues (His242, His244) and Met314, thought to be essential in binding one of the two nonequivalent copper atoms. Substitution of Tyr79 or Tyr318 with Phe increased the Km of PHM for its peptidylglycine substrate without affecting the Vmax. Replacement of Glu313 with Asp increased the Km 8-fold and decreased the kcat 7-fold, again identifying this region of the C-terminal domain as crit. to catalytic activity. Taking into account information on the copper ligands in PHM, we propose a two-domain model with a copper site in each domain that allows spatial proximity between previously described copper ligands and residues identified as catalytically important.

IT 52-90-4, L-Cysteine, biological studies
 (peptidylglycine .alpha.-hydroxylating monooxygenase: active site residues, **disulfide** linkages, and two-domain model of catalytic core)
 RN 52-90-4 HCA
 CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



CC 7-5 (Enzymes)
 ST peptidylglycine alpha hydroxylating monooxygenase active site;
disulfide group peptidylglycine alpha hydroxylating monooxygenase; copper site peptidylglycine alpha hydroxylating monooxygenase
 IT Enzyme functional sites
 (active; peptidylglycine .alpha.-hydroxylating monooxygenase: active site residues, **disulfide** linkages, and two-domain model of catalytic core)
 IT Enzyme functional sites
 (metal-binding; peptidylglycine .alpha.-hydroxylating monooxygenase: active site residues, **disulfide** linkages, and two-domain model of catalytic core)
 IT **Disulfide** group
 (peptidylglycine .alpha.-hydroxylating monooxygenase: active site

- residues, **disulfide** linkages, and two-domain model of catalytic core)
- IT Conformation
(protein; peptidylglycine .alpha.-hydroxylating monooxygenase: active site residues, **disulfide** linkages, and two-domain model of catalytic core)
- IT 52-90-4, L-Cysteine, biological studies 56-86-0, L-Glutamic acid, biological studies 60-18-4, L-Tyrosine, biological studies 71-00-1, L-Histidine, biological studies 90597-47-0, Peptidylglycine .alpha.-Hydroxylating Monooxygenase (peptidylglycine .alpha.-hydroxylating monooxygenase: active site residues, **disulfide** linkages, and two-domain model of catalytic core)
- IT 7440-50-8, Copper, biological studies 15158-11-9, Copper 2+, biological studies (peptidylglycine .alpha.-hydroxylating monooxygenase: active site residues, **disulfide** linkages, and two-domain model of catalytic core)

L99 ANSWER 24 OF 28 HCA COPYRIGHT 2004 ACS on STN

126:340782 Analyses of **disulfides** present in the rubella virus E1 glycoprotein. Gros, Christof; Linder, Monica; Wengler, Gisela; Wengler, Gerd (Institut fur Virologie, Justus-Liebig-Universitat Giessen, Giessen, 35392, Germany). Virology, 230(2), 179-186 (English) 1997. CODEN: VIRLAX. ISSN: 0042-6822. Publisher: Academic.

AB The surface of Rubella virus contains the glycoproteins E1 and E2. The E1 protein induces neutralizing antibodies and has been implicated in the process of recognition of cellular receptors. To gain information on the structural organization of the E1 **protein** we have **analyzed** the **disulfide** bonds present within this mol. The reactivity of the protein with **radioactively** labeled iodoacetic acid indicates that all 20 **cysteine** residues present in the ectodomain of the E1 protein are involved in **disulfide** formation. E1 protein was purified by preparative SDS-PAGE under nonreducing conditions from virus particles grown in tissue culture in the presence of [35S]**cysteine**. The purified protein was **digested** with a no. of proteases followed by reversed phase high-performance liq. chromatog. (HPLC). [35S]**cysteine** -contg. **peptides** were identified and characterized by N-terminal amino acid sequence detn. These analyses identified the following eight **disulfide** bridges: C(1)-C(2); C(3)-C(15); C(6)-C(7); C(9)-C(10); C(11)-C(12); C(13)-C(14); C(17)-C(18); and C(19)-C(20). The two **disulfide** bridges formed by the residues C(4), C(5), C(8), and C(16) have not been identified with certainty, but a likely organization can be derived. The data obtained are discussed in the context of a possible structural and

- functional organization of the E1 protein.
- CC 10-1 (Microbial, Algal, and Fungal Biochemistry)
Section cross-reference(s): 6
- ST rubella virus E1 protein **disulfide**
- IT Glycoproteins, specific or class
(E1; analyses of **disulfides** present in rubella virus E1 glycoprotein)
- IT Conformation
Protein sequences
Rubella virus
(analyses of **disulfides** present in rubella virus E1 glycoprotein)
- IT **Disulfides**
(analyses of **disulfides** present in rubella virus E1 glycoprotein)
- IT Bond
(sulfur-sulfur; analyses of **disulfides** present in rubella virus E1 glycoprotein)
- L99 ANSWER 25 OF 28 HCA COPYRIGHT 2004 ACS on STN
124:254489 Analysis of **disulfide**-containing fragments of Na⁺,K⁺-ATPase. III. Amino acid sequence of cysteinyl **peptides**. Location of **disulfide** bonds of .alpha.-subunit. Gevondyan, N. M.; Gavril'eva, E. E.; Gevondyan, V. S.; Grinberg, A. V.; Modyanov, N. N. (Shemyakin Ovchinnikov Inst. Bioorg. Chem., Moscow, Russia). Biologicheskie Membrany, 12(1), 22-8 (Russian) 1995. CODEN: BIMEE9. ISSN: 0233-4755. Publisher: Nauka.
- AB For localization of **S-S** bonds in the pig kidney Na⁺,K⁺-ATPase .alpha.-subunit, **cysteine**-contg. **peptides** (V-1, VII-1, and VII-2) obtained in the previous study from the enzyme's tryptic **digest** were analyzed. Chem. modification of the **cysteine**-contg. **peptides** performed by **cysteine** residues involved successive alkylations with **radioactive** iodoacetic acid and with ABD-F in the absence and presence of a reducing agent, resp. Cysteinyl **peptides** were isolated by HPLC, their amino acid sequences were detd. and two **disulfide** bonds, Cys452-Cys456 and Cys511-Cys549, were localized by identification of fluorescent **cysteine** residues.
- CC 7-5 (Enzymes)
- ST **disulfide** bond sodium potassium ATPase sequence
- IT **Protein** sequences
(anal. of **disulfide**-contg. fragments of Na⁺,K⁺-ATPase. III. Amino acid sequence of cysteinyl **peptides**. Location of **disulfide** bonds of .alpha.-subunit)
- IT Swine

(anal. of **disulfide**-contg. fragments of pig Na⁺,K⁺-ATPase. III. Amino acid sequence of cysteinyl **peptides**. Location of **disulfide** bonds of .alpha.-subunit)

IT Bond

(sulfur-sulfur, anal. of **disulfide**-contg. fragments of Na⁺,K⁺-ATPase. III. Amino acid sequence of cysteinyl **peptides**. Location of **disulfide** bonds of .alpha.-subunit)

IT 9000-83-3, ATPase

(.alpha. subunit, sodium-potassium-dependent; anal. of **disulfide**-contg. fragments of Na⁺,K⁺-ATPase. III. Amino acid sequence of cysteinyl **peptides**. Location of **disulfide** bonds of the .alpha.-subunit)

L99 ANSWER 26 OF 28 HCA COPYRIGHT 2004 ACS on STN

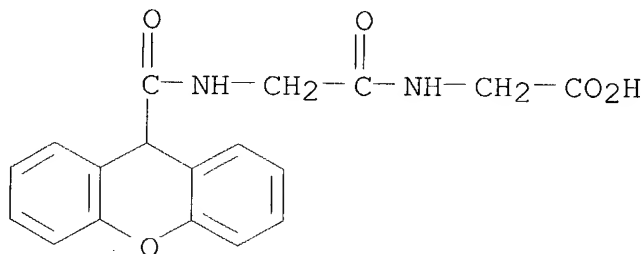
120:293590 Separation method with auxiliary ligand-binder pairs in immunological detection of multiple analytes. Abuknesha, Ramadan Arbi (GEC-Marconi Ltd., UK). PCT Int. Appl. WO 9403807 A1 19940217, 71 pp. DESIGNATED STATES: W: CA, JP, US; RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1993-GB1627 19930802. PRIORITY: GB 1992-16450 19920803; GB 1992-16683 19920806; GB 1992-19743 19920918; GB 1992-20722 19921001; GB 1992-24898 19921127; GB 1992-24897 19921127.

AB A sepn. method which finds application in immunol. detection, a method suitable for use in detection, a sensor, and a test kit are disclosed. The invention provides a sepn. method suitable for use in an immunol. method for the detection of >1 species, which includes the use of >1 auxiliary ligand-binder pairs, the auxiliary ligand of each of the plurality of auxiliary ligand-binder pairs being provided on a support material. The invention also provides a sepn. method which includes the use of a plurality of auxiliary ligand-binder pairs, an auxiliary ligand of one auxiliary ligand-binder pair being provided on a support material and a binder of another auxiliary ligand-binder pair, which pair comprises an auxiliary ligand-auxiliary binder pair, being provided on a support material. The invention is useful for detection of multiple analytes. 17.beta.-Estradiol, progesterone and L-thyroxine were selected as analytes to illustrate the use of >1 auxiliary ligand-auxiliary binder pairs in sepn. of multiple analytes for immunol. detection. The auxiliary ligands used were 7-hydroxy-4-methylcoumarin-3propionic acid, 2-(4-aminophenyl)-6-methylthiazole hemiglutarate, and 2-phenyl-4-quinoline carboxylic acid; auxiliary binders were antibodies to these ligands.

IT 154821-26-8

(as auxiliary ligand, antibody as auxiliary binder to, in sepn. in multiple analyte immunol. detection)

RN 154821-26-8 HCA
 CN Glycine, N-[N-(9H-xanthen-9-ylcarbonyl)glycyl]- (9CI) (CA INDEX NAME)



IT 9003-53-6, Polystyrene
 (support material, auxiliary ligand immobilized on, in sepn. for multiple analyte immunol. detection)
 RN 9003-53-6 HCA
 CN Benzene, ethenyl-, homopolymer (9CI) (CA INDEX NAME)

CM 1

CRN 100-42-5

CMF C8 H8

$\text{H}_2\text{C}=\text{CH}-\text{Ph}$

IC ICM G01N033-537
 ICS G01N033-543; G01N033-58
 CC 9-10 (Biochemical Methods)
 IT Hormones

Proteins, analysis

Steroids, analysis

Thyroid hormones

Toxins

(detection of, immunochem., auxiliary ligand-binder pair in sepn. in)

IT 51-28-5, 2,4-Dinitrophenol, analysis 58-85-5, Biotin 71-63-6, Digitoxin 91-64-5, Coumarin 132-60-5, 2-Phenyl-4-quinoline carboxylic acid 2321-07-5, Fluorescein 14202-13-2, 3-Methyl-1-adamantane acetic acid 18209-43-3 18530-30-8 24327-08-0 53127-08-5, Cibacron Blue 60835-71-4, 4-Amino-benzo-15-crown-5 72088-94-9, Carboxyfluorescein 76079-45-3 81925-04-4 154821-25-7 **154821-26-8** 154821-27-9, 4-Hydroxy-7-trifluoromethyl-3-quinolinedicarboxylic acid (as auxiliary ligand, antibody as auxiliary binder to, in sepn. in multiple analyte immunol. detection)

IT 9003-53-6, Polystyrene

(support material, auxiliary ligand immobilized on, in sepn. for multiple analyte immunol. detection)

L99 ANSWER 27 OF 28 HCA COPYRIGHT 2004 ACS on STN

114:38439 Peptidylchloromethyl ketone substrates for the detection of catalytically active serine proteases by immuno assay. Mann, Kenneth G.; Williams, Brady; Tracy, Russell P. (University of Vermont and State Agricultural College, USA). PCT Int. Appl. WO 9003577 A1 19900405, 55 pp. DESIGNATED STATES: W: JP; RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE. (English). CODEN: PIXXD2. APPLICATION: WO 1989-US4192 19890926. PRIORITY: US 1988-252506 19880930.

AB Substituted peptidyl-chloromethyl ketone derivs. are irreversible inhibitors of serine **proteinases**. The **peptide** (1-3 amino acids) gives the compd. specificity for the active site of a particular **proteinase**. Substitution with a reporting group (e.g. biotin, a fluorophore) allows these substrates to be used in immunoassays for catalytically active serine **proteinases**. These reagents measure active sites rather than cross-reacting material (e.g. zymogens) and are therefore particularly suitable for the **detn.** of serine **proteinase** activity of blood coagulation factors. Biotinyl-.epsilon.-aminocaproyl-D-phenylalanyl-L-prolyl-L-arginine chloromethyl ketone (BC-PPACK) was synthesized by std. chem. and coupled to tissue-type plasminogen activator (tPA) to give tPA-BCPPACK. This was bound to avidin coated microtiter plates and the bound tPA measured by immunoassay using peroxidase-coupled antibody. The std. curve showed a lower limit of sensitivity of 2 ng tPA/mL with test samples of 500 ng tPA/mL accurately measured.

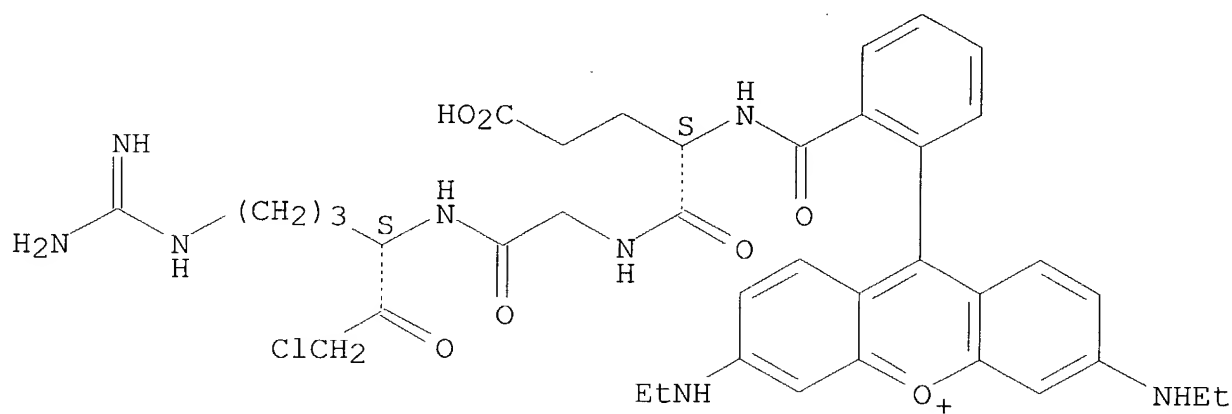
IT 121593-25-7 121606-84-6 130056-27-8
130075-50-2 130404-52-3

(active site-specific fluorescent reagent for serine **proteinases**, immunoassays in relation to)

RN 121593-25-7 HCA

CN Glycinamide, N-[2-[3,6-bis(ethylamino)xanthylum-9-yl]benzoyl]-L-.alpha.-glutamyl-N-[4-[(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]-, chloride, (S)- (9CI) (CA INDEX NAME)

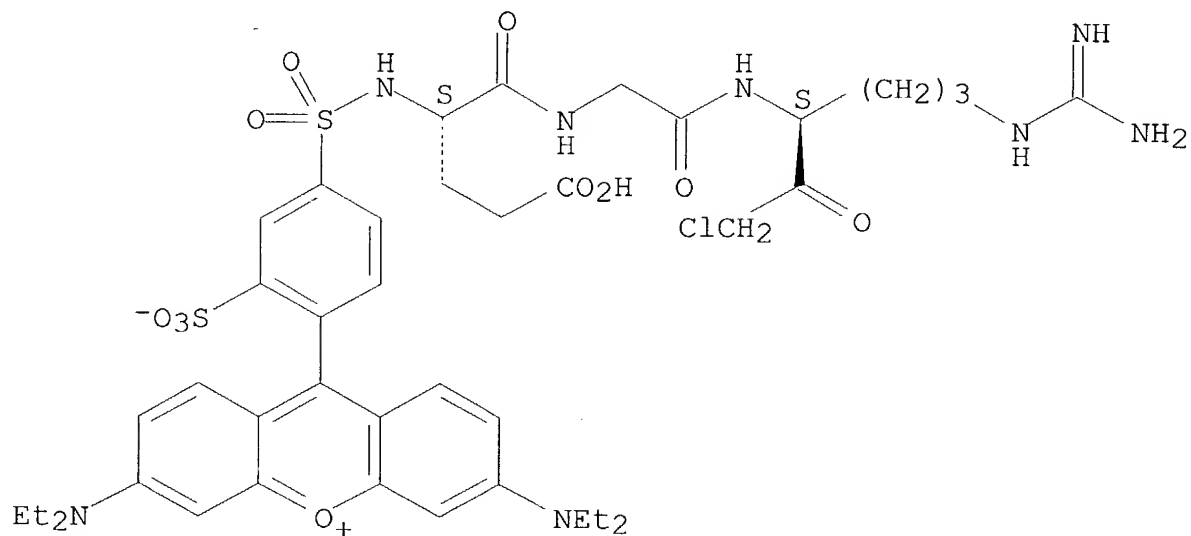
Absolute stereochemistry.



● Cl⁻

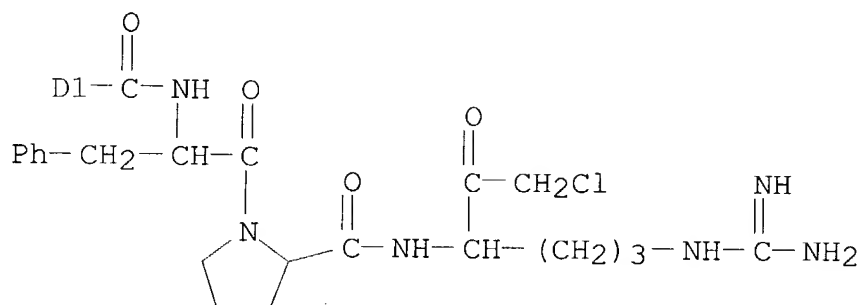
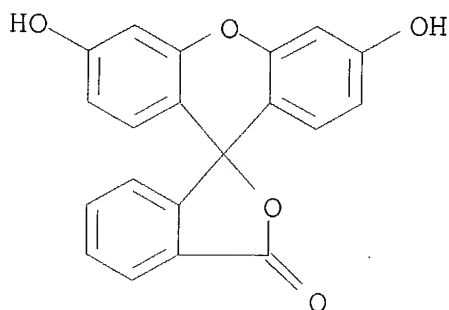
RN 121606-84-6 HCA
 CN Glycinamide, N-[[4-[3,6-bis(diethylamino)xanthylum-9-yl]-3-sulfophenyl]sulfonyl]-L-.alpha.-glutamyl-N-[4-[(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]-, inner salt, (S)-(9CI) (CA INDEX NAME)

Absolute stereochemistry.

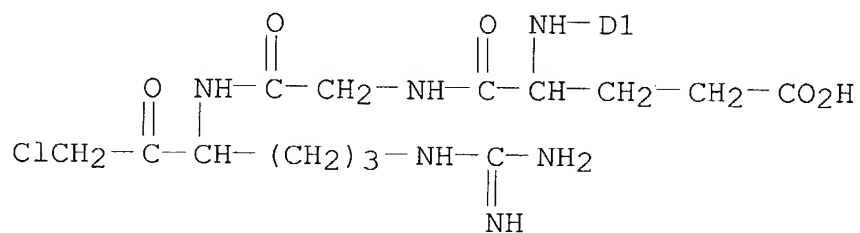
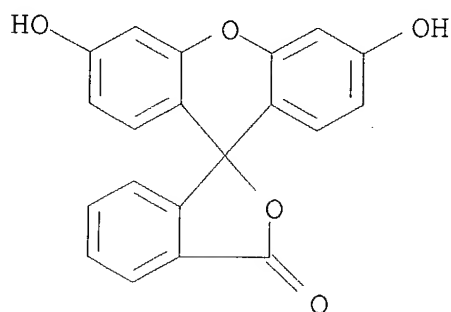


RN 130056-27-8 HCA
 CN L-Prolinamide, N-[[3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-

[9H]xanthen]-5(or 6)-yl]carbonyl]-L-phenylalanyl-N-[4-
[(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]- (9CI) (CA INDEX
NAME)

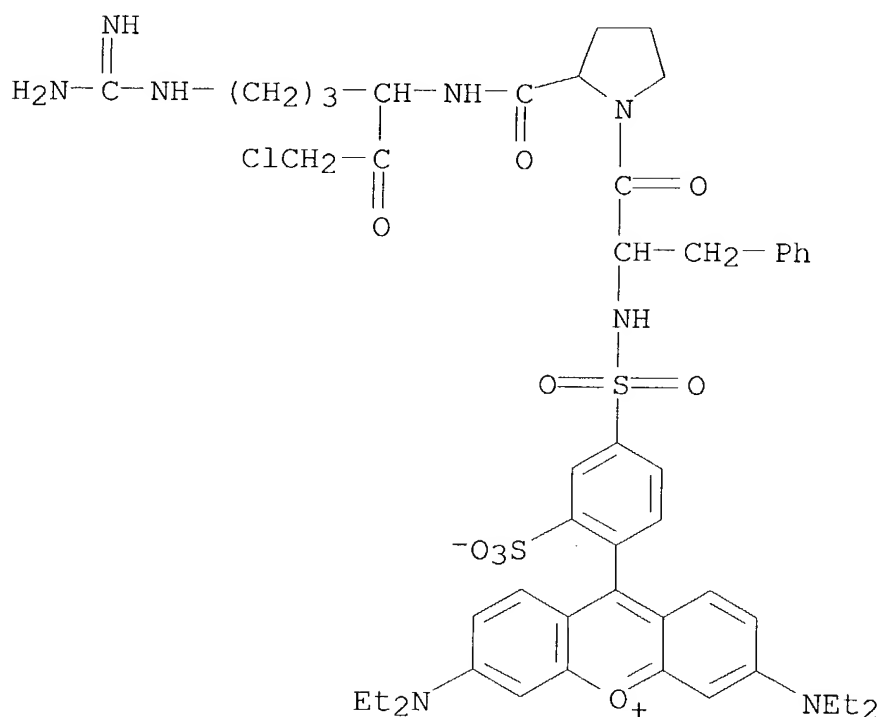


RN 130075-50-2 HCA
CN Glycinamide, N-[3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9']-
[9H]xanthen]-5(or 6)-yl]-L-.alpha.-glutamyl-N-[4-
[(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]-, (S)- (9CI) (CA
INDEX NAME)



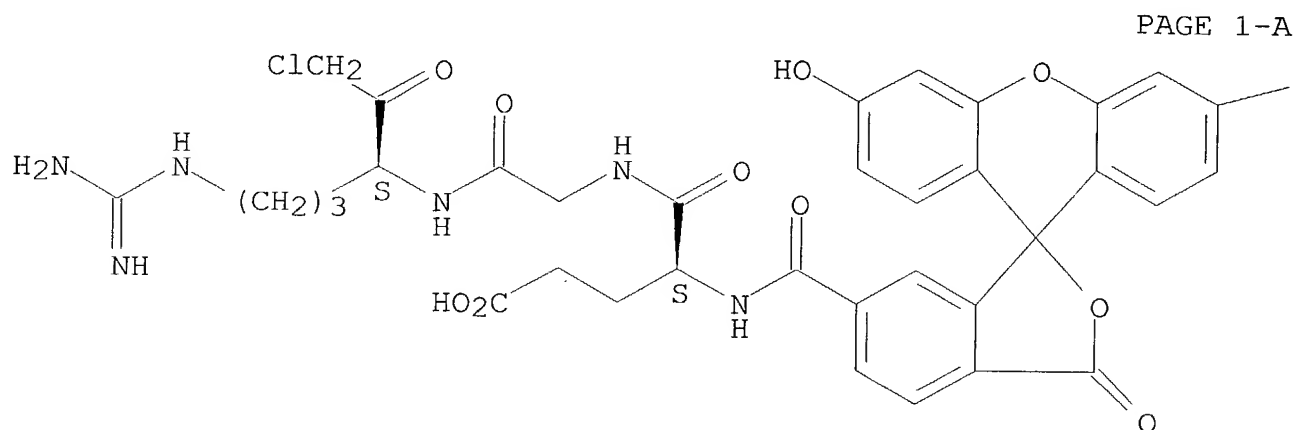
RN 130404-52-3 HCA

CN L-Prolinamide, N-[[4-[3,6-bis(diethylamino)xanthylum-9-yl]-3-sulfophenyl]sulfonyl]-L-phenylalanyl-N-[4-[(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]-, inner salt, (S)- (9CI) (CA INDEX NAME)



IT 121593-21-3P 121596-24-5P
 (prepn. of, as active site-specific fluorescent reagent for
 serine **proteinases**)
 RN 121593-21-3 HCA
 CN Glycinamide, N-[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-
 [9H]xanthen]-6-yl)carbonyl]-L-α-glutamyl-N-[4-
 [(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]-,
 monohydrochloride, (S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.



● HCl

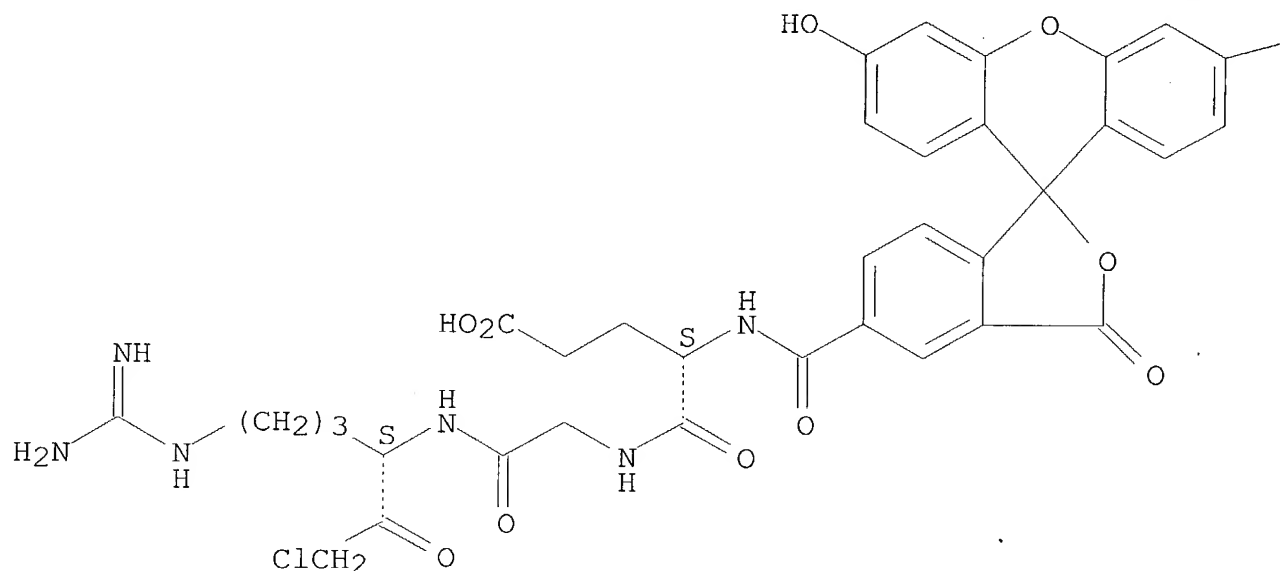
PAGE 1-B

—OH

RN 121596-24-5 HCA
 CN Glycinamide, N-[(3',6'-dihydroxy-3-oxospiro[isobenzofuran-1(3H),9'-[9H]xanthen]-5-yl)carbonyl]-L-.alpha.-glutamyl-N-[4-[(aminoiminomethyl)amino]-1-(chloroacetyl)butyl]-, monohydrochloride, (S)- (9CI) (CA INDEX NAME)

Absolute stereochemistry.

PAGE 1-A



● HCl

PAGE 1-B

- OH
- IC ICM G01N033-573
ICS G01N033-532; G01N033-543; C12Q001-38
- CC 7-3 (Enzymes)
Section cross-reference(s): 9, 13, 15
- ST serine **proteinase** active site **assay** reagent
- IT Immunochemical analysis
(colorimetric active site-specific immunoassay, serine **proteinases detd.** using, active site-specific chloromethyl ketone derivs. in)
- IT Immunochemical **analysis**
(immunoassay, serine **proteinase detn.** using, active site-specific chloromethyl ketone derivs. in)
- IT **Peptides**, compounds
(tri-, chloromethyl ketone analogs, conjugates, with biotin,

- active site-specific reagents for serine **proteinases**,
immunoassays using, blood-coagulation factors in relation to)
- IT 69024-84-6 104302-68-3 121593-24-6 **121593-25-7**
121606-84-6 130056-27-8 130075-50-2
130290-58-3 130325-67-6 130325-68-7 130356-92-2
130404-52-3
(active site-specific fluorescent reagent for serine
proteinases, immunoassays in relation to)
- IT 9001-90-5, Plasmin 9002-04-4, Blood coagulation factor IIa
9002-05-5, Blood coagulation factor Xa 9039-53-6, Urokinase
37259-58-8, Serine **proteinase** 37316-87-3, Blood
coagulation factor IXa 42617-41-4, Blood-coagulation factor XIVA
65312-43-8, Blood coagulation factor VIIA
(**detn.** of, active site-specific chloromethylketones
for, immunoassays using)
- IT 121593-20-2P 130290-57-2P
(prepn. and reactions of, in prepn. serine **proteinase**
active site-specific peptidyl chloromethyl ketones)
- IT **121593-21-3P 121596-24-5P 121606-83-5P**
(prepn. of, as active site-specific fluorescent reagent for
serine **proteinases**)
- IT 130290-54-9P 130290-55-0P
(prepn. of, as active site-specific reagent for **detn.**
of serine **proteinase**)
- IT 121593-23-5P 130290-54-9P 130290-56-1P
(prepn. of, as active site-specific reagent for serine
proteinases)
- IT 56-40-6, Glycine, reactions 109-02-4 543-27-1 2130-96-3
6066-82-6 27601-29-2 35013-72-0 41296-45-1 68715-98-0
71372-26-4 72040-63-2 72088-94-9 82188-90-7 130290-57-2
130325-66-5
(reactions of, in prepn. serine **proteinase** active
site-specific peptidyl chloromethyl ketones)

L99 ANSWER 28 OF 28 HCA COPYRIGHT 2004 ACS on STN

64:69205 Original Reference No. 64:12999h,13000a Variations in amino
acid sequence near the **disulfide** bridges of Bence-Jones
proteins. Milstein, C. (Med. Res. Council Lab. Mol. Biol.,
Cambridge, UK). Nature (London, United Kingdom), 209(5021), 370-3
(English) 1966. CODEN: NATUAS. ISSN: 0028-0836.

AB **Disulfide** bridges of type K Bence-Jones proteins were
quant. reduced and alkylated with iodoacetate-14C. The
radioactive protein was **digested** with trypsin or
chymotrypsin and then fractionated on Sephadex. In the 8
proteins tested, the only variation in the
C-terminal stretch was at position 189 where valine or leucine is
found. The **cysteine** (I) residue toward the N-terminus
showed a stretch of 22 residues after the 1st half of the mol. A

similarity of the sequences around I was found at residue 86 and 23 in some proteins. The 2 variable I residues formed a **disulfide** bridge. Proteins BJ and Rad had a region of variation between positions 90 and 94 with the 5 residues preceding it being identical. The **peptide** with I in position 23 of Bence-Jones was not found in Rad but a different **peptide** around a I residue was found. Protein Ker showed aspartic acid in positions 90 and 91 and the corresponding residues in Bence-Jones and in Rad were glutamic acid and asparagine and glutamic acid and threonine, resp. The heterogeneity of the L-chains of .gamma.-globulin may be the result of the heterogeneity of restricted stretches of the **polypeptide** chain.

CC 56 (General Biochemistry)

IT Proteins

(Bence-Jones, amino acid sequences near **disulfide** bridges of)

IT Amino acids

(in Bence-Jones protein **disulfide** bridge vicinity, sequences of)

IT **Disulfide** group

(in Bence-Jones proteins, amino acid sequences in vicinity of)

=> d 1101 1-28 cbib abs hitstr hitind

L101 ANSWER 1 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:334822 Cloning, sequence and physical characterization of enolase from pathogenic bacteria and their use as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Domagala, Megan; Nethery, Kathleen; Buzadzija, Kristina; Houston, Simon; Ng, Ivy; Vallee, Francois; Awrey, Donald; Beattie, Bryan (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003087352 A2 20031023, 439 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-CA506 20030409. PRIORITY: US 2002-PV371132 20020409; US 2002-PV371365 20020410; US 2002-PV371911 20020411.

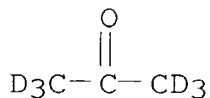
AB The present invention relates to novel drug targets for pathogenic bacteria. The nucleic acid and amino acid sequences are provided for enolases from *Staphylococcus aureus*, *Helicobacter pylori*, and *Streptococcus pneumoniae*. The invention also provides bioinformatic, biochem. and biophys. characteristics of those

polypeptides, in particular characterization by mass spectrometry, NMR spectrometry, and x-ray crystallog.

IT 7782-39-0, Hydrogen-2, uses
 (NMR isotope; cloning, sequence and phys.
 characterization of enolase from pathogenic bacteria and their
 use as antimicrobial targets)
 RN 7782-39-0 HCA
 CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

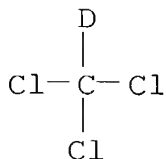
IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
 Methanol-d4 865-49-6, Chloroform-d 1076-43-3,
 Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5
 1693-74-9 2037-26-5 2206-26-0,
 Acetonitrile-d3 2206-27-1 2679-89-2
 4472-41-7 7291-22-7, Pyridine-d5 7789-20-0
 , Heavy water 17222-37-6
 (deuterium lock solvent; cloning, sequence and phys.
 characterization of enolase from pathogenic bacteria and their
 use as antimicrobial targets)
 RN 666-52-4 HCA
 CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



RN 811-98-3 HCA
 CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

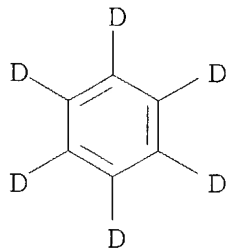
D₃C-O-D

RN 865-49-6 HCA
 CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



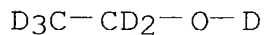
RN 1076-43-3 HCA

CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



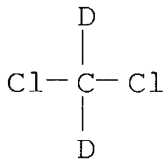
RN 1516-08-1 HCA

CN Ethanol-d6 (9CI) (CA INDEX NAME)



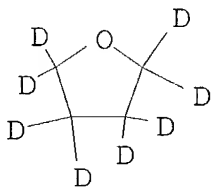
RN 1665-00-5 HCA

CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



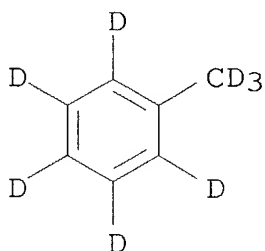
RN 1693-74-9 HCA

CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

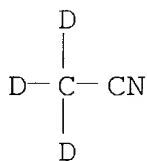


RN 2037-26-5 HCA

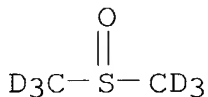
CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



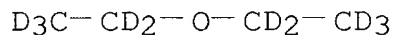
RN 2206-26-0 HCA
 CN Acetonitrile-d3 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



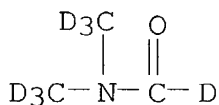
RN 2206-27-1 HCA
 CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



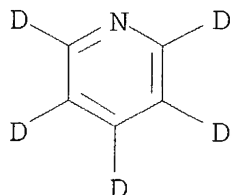
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)

D—O—D

RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)

D₃C—O—CD₃

IC ICM C12N009-00
 CC 7-2 (Enzymes)
 Section cross-reference(s): 1, 3, 10, 75
 IT Antibacterial agents
 Conformation
 Cryoprotectants
 Crystal growth
 DNA sequences
 Drug targets
 Epitopes
 Helicobacter pylori
Mass spectrometry
 Molecular cloning
 NMR spectroscopy
 Pathogenic bacteria
 Protein sequences
 Staphylococcus aureus
 Streptococcus pneumoniae
 X-ray diffractometry
 (cloning, sequence and phys. characterization of enolase from
 pathogenic bacteria and their use as antimicrobial targets)
 IT **Polyoxyalkylenes**, uses
 (low-mol.-wt., cryoprotectant; cloning, sequence and phys.
 characterization of enolase from pathogenic bacteria and their
 use as antimicrobial targets)
 IT Gel electrophoresis
 (protein purity detn.; cloning, sequence and

- phys. characterization of enolase from pathogenic bacteria and their use as antimicrobial targets)
- IT 1333-74-0, Hydrogen, uses 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses **7782-39-0**, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses (NMR **isotope**; cloning, sequence and phys. characterization of enolase from pathogenic bacteria and their use as antimicrobial targets)
- IT 110-82-7, Cyclohexane, uses **666-52-4**, 2-Propanone-1,1,1,3,3,3-d6 **811-98-3**, Methanol-d4 **865-49-6**, Chloroform-d **1076-43-3**, Benzene-d6 **1516-08-1**, Ethanol-d6 **1665-00-5** **1693-74-9** **2037-26-5** **2206-26-0**, Acetonitrile-d3 **2206-27-1** **2679-89-2** **4472-41-7** **7291-22-7**, Pyridine-d5 **7789-20-0**, Heavy water **17222-37-6** (deuterium lock solvent; cloning, sequence and phys. characterization of enolase from pathogenic bacteria and their use as antimicrobial targets)
- IT 25322-68-3, **PEG** (low-mol.-wt., cryoprotectant; cloning, sequence and phys. characterization of enolase from pathogenic bacteria and their use as antimicrobial targets)
- IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs. (mass spectrometry matrix; cloning, sequence and phys. characterization of enolase from pathogenic bacteria and their use as antimicrobial targets)

L101 ANSWER 2 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319353 Cloning and physical characterization of microbial **polypeptides** involved in nucleotide transport and metabolism and their use as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Domagala, Megan; Mansoury, Kamran; Houston, Simon; Awrey, Donald; Beattie, Bryan; Kanagarajah, Dhushy; Vallee, Francois; Virag, Cristina; Buzadzija, Kristina; Mcdonald, Merry-Lynn; Tai, Matthew; Pinder, Benjamin; Alam, Muhammad Zahoor; Ouyang, Hui; Richards, Dawn; Canadien, Veronica; Thalakada, Rosanne; Nethery, Kathleen (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003087354 A2 20031023, 392 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE,

IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English).
CODEN: PIXXD2. APPLICATION: WO 2003-CA485 20030408. PRIORITY: US
2002-PV371067 20020409; US 2002-PV386548 20020605; US 2002-PV386869
20020606; US 2002-PV386826 20020606; US 2002-PV424380 20021106; US
2002-PV425086 20021108; US 2002-PV436288 20021224; US 2002-PV436243
20021224; US 2002-PV436567 20021226; US 2002-PV436566 20021226; US
2002-PV436708 20021227; US 2002-PV437038 20021230; US 2002-PV436971
20021230; US 2002-PV437141 20021230; US 2002-PV436947 20021230; US
2002-PV437638 20021231; US 2002-PV437620 20021231.

AB The present invention relates to **polypeptide** targets for
pathogenic bacteria. Reliable, high throughput methods are
developed to identify, express, and purify a no. of antimicrobial
targets from Staphylococcus aureus, Escherichia coli, Streptococcus
pneumoniae, Enterococcus faecalis, Haemophilus influenzae, and
Pseudomonas aeruginosa. The nucleic acid and amino acid sequences
are provided for dUTPase, guanylate kinase, adenine
phosphoribosyltransferase, thymidylate synthase, uridylate kinase,
ribose phosphate pyrophosphokinase, and cytidine/deoxycytidylate
deaminase family protein. The invention also provides
bioinformatic, biochem. and biophys. characteristics of those
polypeptides, in particular characterization by **mass**
spectrometry, **NMR spectrometry**, and x-ray
crystallog.

IT 7782-39-0, Hydrogen-2, uses
(NMR **isotope**; cloning and phys. characterization of
microbial **polypeptides** involved in nucleotide transport
and metab. and their use as antimicrobial targets)

RN 7782-39-0 HCA

CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

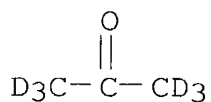
D-D

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 917-96-4,
Methyl-d3 isocyanide 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
2037-26-5 2206-27-1, Dimethyl sulfoxide-d6
2679-89-2, Diethyl-d10 ether 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6,
Dimethyl-d6 ether

(**deuterium** lock solvent for NMR spectroscopy; cloning
and phys. characterization of microbial **polypeptides**
involved in nucleotide transport and metab. and their use as
antimicrobial targets)

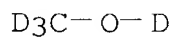
RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



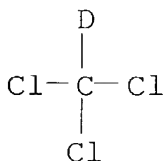
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



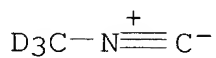
RN 865-49-6 HCA

CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



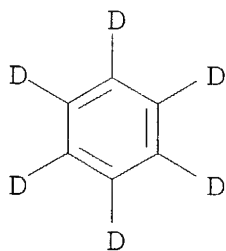
RN 917-96-4 HCA

CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



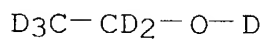
RN 1076-43-3 HCA

CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)

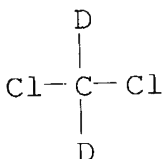


RN 1516-08-1 HCA

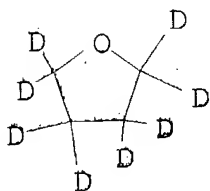
CN Ethanol-d6 (9CI) (CA INDEX NAME)



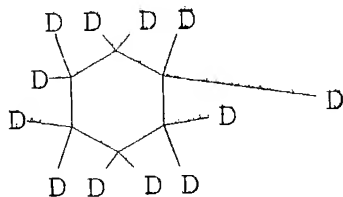
RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



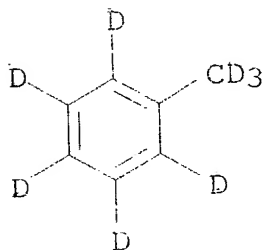
RN 1693-74-9 HCA
CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



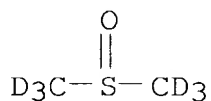
RN 1735-17-7 HCA
CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



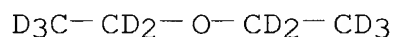
RN 2037-26-5 HCA
CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



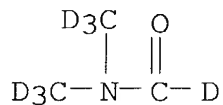
RN 2206-27-1 HCA
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



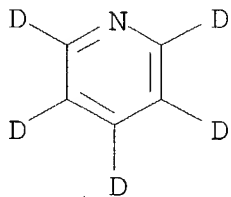
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



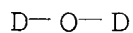
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



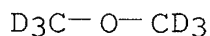
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IC ICM C12N009-14
 ICS C12N015-55
 CC 7-2 (Enzymes)
 Section cross-reference(s): 1, 3, 6, 10
 ST essential protein pathogenic bacteria therapeutic target; sequence

- essential protein gene pathogenic bacteria; **mass spectrometry** essential **protein** pathogenic bacteria; NMR **spectrometry** essential **protein** pathogenic bacteria; xray crystallog essential protein pathogenic bacteria; cloning essential protein pathogenic bacteria
- IT Molecular chaperones
(DnaK, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT Molecular chaperones
(GroEL, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT Antibacterial agents
Cryoprotectants
Crystallization
DNA sequences
Drug design
Drug screening
Drug targets
Enterococcus faecalis
Epitopes
Escherichia coli
Haemophilus influenzae
Mass spectrometry
Molecular cloning
NMR spectroscopy
Pathogenic bacteria
Protein sequences
Pseudomonas aeruginosa
Staphylococcus aureus
Streptococcus pneumoniae
(cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT Hydrocarbon oils
Polyoxyalkylenes, uses
(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT Solvents
(**deuterium** lock, for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT Fusion proteins (chimeric proteins)

(for improved soly. or stability; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT Elements

(heavy, for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT Proteins

(in nucleotide transport and metab.; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT Molecular association

(protein-protein; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT Nucleotides, biological studies

(proteins involved in transport and metab. of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT Crystallography

(x-ray; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses **7782-39-0**, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses

(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT 612552-95-1P 612552-98-4P 612553-00-1P 612553-02-3P
612553-04-5P 612553-06-7P 612553-09-0P 612553-11-4P
612553-13-6P 612553-15-8P 612553-17-0P 612553-19-2P
612553-21-6P 612553-23-8P 612553-26-1P 612553-28-3P
612553-30-7P 612553-32-9P 612553-34-1P 612553-36-3P
612553-39-6P 612553-41-0P

(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT 9015-83-2P, Ribose phosphate pyrophosphokinase 9026-59-9P, Guanylate kinase 9027-80-9P, Adenine phosphoribosyltransferase 9031-61-2P, Thymidylate synthase 9036-23-1P, Uridylate kinase 37289-34-2P

- (cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0, Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3, **Polyethylene glycol** (cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6, Chloroform-d 917-96-4, Methyl-d3 isocyanide 1076-43-3, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6 2679-89-2, Diethyl-d10 ether 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, Deuterium oxide 17222-37-6, Dimethyl-d6 ether (deuterium lock solvent for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT 9025-06-3P, Cytidine deaminase 9026-92-0P, Deoxycytidylate deaminase (family member; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)
- IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9, Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses 7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7, Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium, uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses 7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses 7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9, Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium, uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses 7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4, Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses 7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1, Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses (heavy atom for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides**)

involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs.

(mass spectrometry of; cloning and phys.

characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT 612552-94-0, DNA (Streptococcus pneumoniae gene dut) 612552-96-2, DNA (Streptococcus pneumoniae gene dut) 612552-97-3, DNA (Staphylococcus aureus gene gmk) 612552-99-5, DNA (Pseudomonas aeruginosa gene APT) 612553-01-2, DNA (Pseudomonas aeruginosa gene PRSA) 612553-03-4, DNA (Pseudomonas aeruginosa gene PRSA) 612553-05-6, DNA (Pseudomonas aeruginosa gene gmk) 612553-07-8, DNA (Pseudomonas aeruginosa gene gmk) 612553-08-9, DNA (Enterococcus faecalis gene thyA) 612553-10-3, DNA (Enterococcus faecalis gene thyA) 612553-12-5, DNA (Enterococcus faecalis gene PYRH) 612553-14-7, DNA (Escherichia coli gene gmk) 612553-16-9, DNA (Enterococcus faecalis gene APT) 612553-18-1, DNA (Enterococcus faecalis gene APT) 612553-20-5, DNA (Enterococcus faecalis gene gmk) 612553-22-7, DNA (Enterococcus faecalis gene PRSA) 612553-24-9, DNA (Enterococcus faecalis gene PRSA) 612553-25-0, DNA (Haemophilus influenzae gene KTHY) 612553-27-2, DNA (Haemophilus influenzae gene KTHY) 612553-29-4, DNA (Haemophilus influenzae gene APT) 612553-31-8, DNA (Haemophilus influenzae gene gmk) 612553-33-0, DNA (Haemophilus influenzae gene gmk) 612553-35-2, DNA (Pseudomonas aeruginosa gene KTHY) 612553-37-4, DNA (Pseudomonas aeruginosa gene KTHY) 612553-38-5, DNA (Streptococcus pneumoniae gene KTHY) 612553-40-9, DNA (Streptococcus pneumoniae gene YHFC) 612553-42-1, DNA (Streptococcus pneumoniae gene YHFC)

(nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT 3211-76-5, Selenomethionine

(protein label for mass spectrometry; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT	612572-78-8	612572-79-9	612572-80-2	612572-81-3	612572-82-4
	612572-83-5	612572-84-6	612572-85-7	612572-86-8	612572-87-9
	612572-88-0	612572-89-1	612572-91-5	612572-92-6	612572-93-7
	612572-94-8	612572-95-9	612572-96-0	612572-97-1	612572-98-2
	612573-00-9	612573-01-0	612573-02-1	612573-03-2	612573-04-3
	612573-05-4	612573-06-5	612573-07-6	612573-08-7	612573-09-8
	612573-10-1	612573-11-2	612573-12-3	612573-13-4	

(unclaimed nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in

nucleotide transport and metab. and their use as antimicrobial targets)

IT 612572-90-4 612572-99-3
(unclaimed protein sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

IT 612512-63-7 612512-64-8 612512-65-9 612512-66-0 612512-67-1
612512-68-2 612512-69-3 612512-70-6 612512-71-7 612512-72-8
612512-73-9 612512-74-0 612512-75-1 612512-76-2 612512-77-3
612512-78-4 612512-79-5 612512-80-8 612512-81-9 612512-82-0
612512-83-1 612512-84-2 612512-85-3 612512-86-4 612512-87-5
612512-88-6 612512-89-7 612512-90-0 612512-91-1 612512-92-2
612512-93-3 612512-94-4 612512-95-5 612512-96-6 612512-97-7
612512-98-8 612512-99-9 612513-00-5 612513-01-6 612513-02-7
612513-03-8 612513-04-9 612513-05-0 612513-06-1 612513-07-2
612513-08-3 612513-09-4 612513-10-7

(unclaimed sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide transport and metab. and their use as antimicrobial targets)

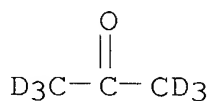
L101 ANSWER 3 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319352 Cloning and physical characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Domagala, Megan; Houston, Simon; Awrey, Donald; Beattie, Bryan; Mansoury, Kamran; Ouyang, Hui; Vallee, Francois; Richards, Dawn; Nethery, Kathleen; Virag, Cristina; Buzadzija, Kristina; Pinder, Benjamin; Alam, Muhammad Zahoor; Tai, Matthew; Canadien, Veronica; Kanagarajah, Dhushy; Thalakada, Rosanne (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003087353 A2 20031023, 407 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-CA481 20030408. PRIORITY: US 2002-PV370915 20020408; US 2002-PV370899 20020408; US 2002-PV371185 20020409; US 2002-PV371107 20020409; US 2002-PV385426 20020531; US 2002-PV386283 20020606; US 2002-PV400348 20020801; US 2002-PV424395 20021106; US 2002-PV425200 20021108; US 2002-PV436345 20021224; US 2002-PV436349 20021224; US 2002-PV436568 20021226; US 2002-PV436893 20021227; US 2002-PV436889 20021227; US 2002-PV436675 20021227; US 2002-PV436900 20021227; US 2002-PV436885 20021227; US 2002-PV436734 20021227; US 2002-PV437013 20021230.

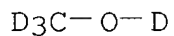
- AB The present invention relates to **polypeptide** targets for pathogenic bacteria. Reliable, high throughput methods are developed to identify, express, and purify a no. of antimicrobial targets from Staphylococcus aureus, Escherichia coli, Streptococcus pneumoniae, Enterococcus faecalis, Haemophilus influenzae, and Pseudomonas aeruginosa. The nucleic acid and amino acid sequences are provided for UDP-acetylglucosamine 1-carboxyvinyltransferase 1, CTP: CMP-3-deoxy-D-mannoctulosonate transferase, UDP-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase, D-alanine:D-alanine-adding enzyme, D-alanine:D-alanine ligase, UDP-acetylpyruvoylglucosamine reductase,, UDP-acetylglucosamine pyrophosphorylase, UDP-acetylmuramoylalanine-D-glutamate ligase, UDP-acetylmuramate:alanine ligase, and aspartate semialdehyde dehydrogenase. The invention also provides bioinformatic, biochem. and biophys. characteristics of those **polypeptides**, in particular characterization by **mass spectrometry**, **NMR spectrometry**, and x-ray crystallog.
- IT 7782-39-0, Hydrogen-2, uses
(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)
- RN 7782-39-0 HCA
- CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

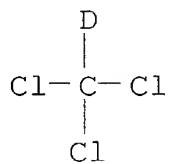
- IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 917-96-4,
Methyl-d3 isocyanide 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
2037-26-5 2206-27-1, Dimethyl sulfoxide-d6
2679-89-2, Diethyl-d10 ether 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6,
Dimethyl-d6 ether
(**deuterium** lock solvent for NMR spectroscopy; cloning
and phys. characterization of microbial **polypeptides**
involved in membrane biogenesis and their use as antimicrobial
targets)
- RN 666-52-4 HCA
- CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



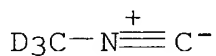
RN 811-98-3 HCA
CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



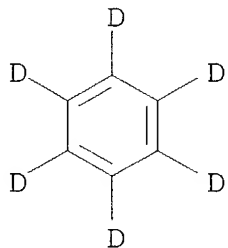
RN 865-49-6 HCA
CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



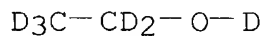
RN 917-96-4 HCA
CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



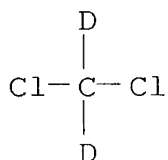
RN 1076-43-3 HCA
CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



RN 1516-08-1 HCA
CN Ethanol-d6 (9CI) (CA INDEX NAME)

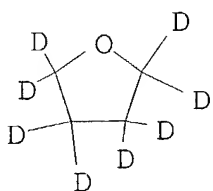


RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



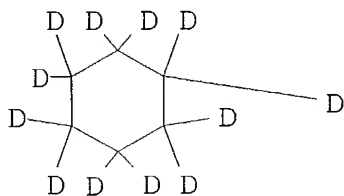
RN 1693-74-9 HCA

CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



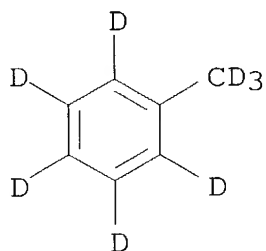
RN 1735-17-7 HCA

CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



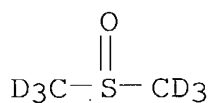
RN 2037-26-5 HCA

CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)

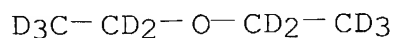


RN 2206-27-1 HCA

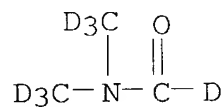
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



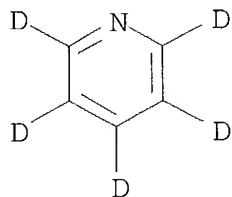
RN 2679-89-2 HCA
CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



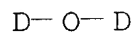
RN 4472-41-7 HCA
CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



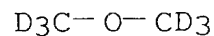
RN 7291-22-7 HCA
CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IC ICM C12N009-10
CC 7-2 (Enzymes)
Section cross-reference(s): 1, 3, 6, 10
ST essential protein pathogenic bacteria therapeutic target; sequence
essential protein gene pathogenic bacteria; **mass**

- spectrometry essential protein pathogenic
bacteria; NMR spectrometry essential protein
pathogenic bacteria; xray crystallog essential protein pathogenic
bacteria; cloning essential protein pathogenic bacteria
- IT Heat-shock proteins
(HSP 70, protein-protein interactions of; cloning and phys.
characterization of microbial **polypeptides** involved in
membrane biogenesis and their use as antimicrobial targets)
- IT Ribosomal proteins
(L2, protein-protein interactions of; cloning and phys.
characterization of microbial **polypeptides** involved in
membrane biogenesis and their use as antimicrobial targets)
- IT Enzymes, biological studies
(RNA helicase, ATP-dependent, protein-protein interactions of;
cloning and phys. characterization of microbial
polypeptides involved in membrane biogenesis and their
use as antimicrobial targets)
- IT Ribosomal proteins
(S1, protein-protein interactions of; cloning and phys.
characterization of microbial **polypeptides** involved in
membrane biogenesis and their use as antimicrobial targets)
- IT Ribosomal proteins
(S10, protein-protein interactions of; cloning and phys.
characterization of microbial **polypeptides** involved in
membrane biogenesis and their use as antimicrobial targets)
- IT Antibacterial agents
Cryoprotectants
Crystallization
DNA sequences
Drug design
Drug screening
Drug targets
Enterococcus faecalis
Epitopes
Escherichia coli
Haemophilus influenzae
Mass spectrometry
Molecular cloning
NMR spectroscopy
Pathogenic bacteria
Protein sequences
Pseudomonas aeruginosa
Staphylococcus aureus
Streptococcus pneumoniae
(cloning and phys. characterization of microbial
polypeptides involved in membrane biogenesis and their
use as antimicrobial targets)
- IT Hydrocarbon oils

Polyoxyalkylenes, uses

(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Solvents

(**deuterium** lock, for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Fusion proteins (chimeric proteins)

(for improved soly. or stability; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Elements

(heavy, for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Proteins

(in membrane biogenesis; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Flagellins

(protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Molecular association

(protein-protein; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Membrane, biological

(proteins involved in biogenesis of; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT Crystallography

(x-ray; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses

7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses

7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses

12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4,

Carbon-13, uses

(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 612553-71-6P 612553-77-2P 612553-78-3P 612553-80-7P

612553-82-9P 612553-84-1P 612553-86-3P 612553-88-5P

612553-89-6P 612553-90-9P 612553-91-0P 612553-92-1P
 612553-94-3P 612553-96-5P 612553-98-7P 612554-00-4P
 612554-02-6P 612554-04-8P 612554-06-0P 612554-08-2P
 612554-09-3P 612554-10-6P 612554-11-7P 612554-12-8P
 612554-13-9P 612554-14-0P 612554-15-1P 612554-16-2P
 612554-17-3P 612554-18-4P 612554-20-8P 612854-64-5P
 612854-66-7P

(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 612553-73-8 612553-75-0

(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 9000-98-0P, Aspartate semialdehyde dehydrogenase 9023-06-7P,
 UDP-acetylglucosamine pyrophosphorylase 9023-27-2P,
 UDP-N-acetylglucosamine 1-carboxyvinyltransferase 9023-52-3P,
 UDP-N-acetylmuramate:L-alanine ligase 9023-59-0P,
 UDP-N-acetylmuramoylalanine-D-glutamate ligase 9023-63-6P,
 D-Alanine:D-alanine ligase 9075-09-6P, UDP-N-acetylmuramyl-L-alanyl-D-glutamate:2,6-diaminopimelate ligase 37278-28-7P,
 CTP: CMP-3-deoxy-mannoctulosonate cytidyltransferase 39307-28-3P, UDP-acetylenolpyruvylglucosamine reductase 55354-36-4P, D-Alanyl-D-alanine-adding enzyme

(cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0, Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3, **Polyethylene glycol**

(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6, Chloroform-d 917-96-4, Methyl-d3 isocyanide 1076-43-3, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6 2679-89-2, Diethyl-d10 ether 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, Deuterium oxide 17222-37-6, Dimethyl-d6 ether

(deuterium lock solvent for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

- IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9, Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses 7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7, Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium, uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses 7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses 7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9, Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium, uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses 7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4, Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses 7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1, Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses (heavy atom for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)
- IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs. (mass spectrometry of; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)
- IT 612553-74-9P, DNA (Staphylococcus aureus gene murA) (nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)
- IT 612553-70-5, DNA (Pseudomonas aeruginosa gene murA) 612553-72-7, DNA (Pseudomonas aeruginosa gene murA) 612553-79-4, DNA (Escherichia coli gene kdsB) 612553-81-8, DNA (Escherichia coli gene kdsB) 612553-83-0, DNA (Haemophilus pneumoniae gene kdsB) 612553-85-2, DNA (Pseudomonas aeruginosa gene murE) 612553-87-4, DNA (Pseudomonas aeruginosa gene murE) 612553-93-2, DNA (Pseudomonas aeruginosa gene murF) 612553-95-4, DNA (Pseudomonas aeruginosa gene murF) 612553-97-6, DNA (Enterococcus faecalis gene ddlA) 612553-99-8, DNA (Enterococcus faecalis gene ddlA) 612554-01-5, DNA (Pseudomonas aeruginosa gene murB) 612554-03-7, DNA (Pseudomonas aeruginosa gene murB) 612554-05-9, DNA (Haemophilus influenzae gene murB) 612554-07-1, DNA (Haemophilus influenzae gene murB) 612554-19-5, DNA (Haemophilus influenzae gene asd) 612854-49-6, DNA (Streptococcus pneumoniae gene murA) 612854-50-9, DNA (Streptococcus pneumoniae gene murA) 612854-51-0, DNA (Haemophilus influenzae gene murE) 612854-52-1, DNA (Haemophilus influenzae gene murE) 612854-53-2, DNA (Staphylococcus aureus gene murF) 612854-54-3, DNA (Staphylococcus

aureus gene murF) 612854-55-4, DNA (Enterococcus faecalis gene glmU) 612854-56-5, DNA (Enterococcus faecalis gene glmU) 612854-57-6, DNA (Haemophilus influenzae gene glmU) 612854-58-7, DNA (Haemophilus influenzae gene glmU) 612854-59-8, DNA (Staphylococcus aureus gene glmU) 612854-60-1, DNA (Staphylococcus aureus gene glmU) 612854-61-2, DNA (Enterococcus faecalis gene murD) 612854-62-3, DNA (Enterococcus faecalis gene murD) 612854-63-4, DNA (Haemophilus influenzae gene murD) 612854-65-6, DNA (Haemophilus influenzae gene murD) 612854-67-8, DNA (Escherichia coli gene murC) 612854-68-9, DNA (Escherichia coli gene murC)

(nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 3211-76-5, Selenomethionine

(protein label for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 9014-08-8, Enolase 9027-73-0, 5'-Nucleotidase 9027-80-9, Adenine phosphoribosyltransferase

(protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT	612553-76-1	612572-39-1	612572-40-4	612572-41-5	612572-42-6
	612572-43-7	612572-44-8	612572-45-9	612572-46-0	612572-47-1
	612572-48-2	612572-49-3	612572-50-6	612572-51-7	612572-52-8
	612572-53-9	612572-54-0	612572-55-1	612572-56-2	612572-57-3
	612572-58-4	612572-59-5	612572-60-8	612572-61-9	612572-62-0
	612572-63-1	612572-64-2	612572-65-3	612572-66-4	612572-67-5
	612572-68-6	612572-69-7	612572-70-0	612572-71-1	612572-72-2
	612572-74-4	612572-75-5	612572-76-6	612572-77-7	

(unclaimed nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT 612572-73-3

(unclaimed protein sequence; cloning and phys. characterization of microbial **polypeptides** involved in membrane biogenesis and their use as antimicrobial targets)

IT	612542-37-7	612542-38-8	612542-39-9	612542-40-2	612542-41-3
	612542-42-4	612542-43-5	612542-44-6	612542-45-7	612542-46-8
	612542-47-9	612542-48-0	612542-49-1	612542-50-4	612542-51-5
	612542-52-6	612542-53-7	612542-54-8	612542-55-9	612542-56-0
	612542-57-1	612542-58-2	612542-60-6	612542-61-7	612542-62-8
	612542-63-9	612542-64-0	612542-65-1	612542-66-2	612542-67-3
	612542-68-4	612542-69-5	612542-70-8	612542-71-9	612542-72-0
	612542-73-1	612542-74-2	612542-75-3	612542-76-4	612542-77-5
	612542-78-6	612542-79-7	612542-80-0	612542-81-1	612542-82-2

612542-83-3 612542-84-4 612542-85-5 612542-87-7 612542-89-9
612542-91-3 612542-93-5 612542-94-6 612542-95-7 612542-96-8
612542-97-9

(unclaimed sequence; cloning and phys. characterization of
microbial **polypeptides** involved in membrane biogenesis
and their use as antimicrobial targets)

L101 ANSWER 4 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319350 Cloning and physical characterization of microbial
polypeptides involved in cellular transport and metabolism
and their use as antimicrobial targets. Edwards, Aled; Dharamsi,
Akil; Vedadi, Masoud; Li, Qin; Nethery, Kathleen; Mcdonald,
Merry-lynn; Vallee, Francois; Awrey, Donald; Beattie, Bryan;
Domagala, Megan; Mansoury, Kamran; Alam, Muhammad Zahoor; Ng, Ivy;
Ouyang, Hui (Affinium Pharmaceuticals, Inc., Can.; et al.). PCT
Int. Appl. WO 2003087146 A2 20031023, 204 pp. DESIGNATED STATES: W:
AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO,
CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU,
LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO,
RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ,
VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT,
BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR,
IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English).
CODEN: PIXXD2. APPLICATION: WO 2003-CA482 20030408. PRIORITY: US
2002-PV370868 20020408; US 2002-PV371025 20020409; US 2002-PV371094
20020409; US 2002-PV370959 20020409; US 2002-PV371065 20020409.

AB The present invention relates to **polypeptide** targets for
pathogenic bacteria. Reliable, high throughput methods are
developed to identify, express, and purify a no. of antimicrobial
targets from Staphylococcus aureus, Escherichia coli, and
Helicobacter pylori. The nucleic acid and amino acid sequences are
provided for adenylate kinase, UDP-N-acetylglucosamine
pyrophosphorylase, geranyltransferase (farnesyldiphosphate
synthase), enoyl-(acyl carrier protein) reductase (NADH), and
ribonucleoside diphosphate reductase .beta. subunit. The invention
also provides bioinformatic, biochem. and biophys. characteristics
of those **polypeptides**, in particular characterization by
mass spectrometry, **NMR spectrometry**, and
x-ray crystallog.

IT 7782-39-0, Hydrogen-2, uses
(NMR **isotope**; cloning and phys. characterization of
microbial **polypeptides** involved in cellular transport
and metab. and their use as antimicrobial targets)

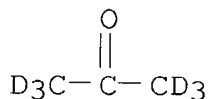
RN 7782-39-0 HCA

CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

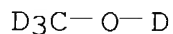
D-D

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
 Methanol-d4 865-49-6, Chloroform-d 917-96-4,
 Methyl-d3 isocyanide 1076-43-3, Benzene-d6
 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
 , Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6
 2679-89-2, Diethyl-d10 ether 4472-41-7,
 N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
 7789-20-0, Deuterium oxide 17222-37-6,
 Dimethyl-d6 ether
 (deuterium lock solvent for NMR spectroscopy; cloning
 and phys. characterization of microbial **polypeptides**
 involved in cellular transport and metab. and their use as
 antimicrobial targets)

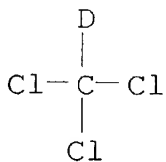
RN 666-52-4 HCA
 CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



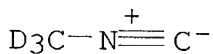
RN 811-98-3 HCA
 CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



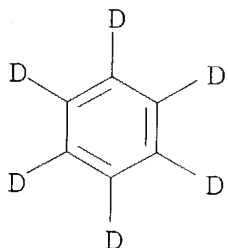
RN 865-49-6 HCA
 CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



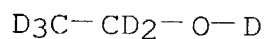
RN 917-96-4 HCA
 CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



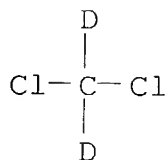
RN 1076-43-3 HCA
CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



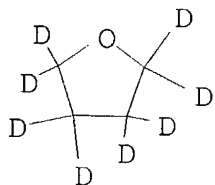
RN 1516-08-1 HCA
CN Ethanol-d6 (9CI) (CA INDEX NAME)



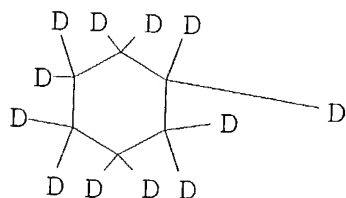
RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



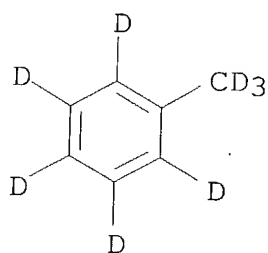
RN 1693-74-9 HCA
CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



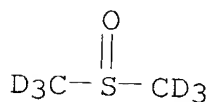
RN 1735-17-7 HCA
CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



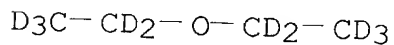
RN 2037-26-5 HCA
 CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



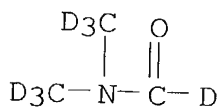
RN 2206-27-1 HCA
 CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



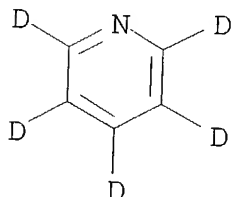
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)

D-O-D

RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)

D₃C-O-CD₃

IC ICM C07K014-31
 ICS C07K014-245; C07K014-205; C12N015-31; C12N015-62; C12Q001-68;
 C12N015-11; C07K016-12; A61K038-16; A61K039-108; A61K039-085;
 A61K039-106
 CC 7-2 (Enzymes)
 Section cross-reference(s): 1, 3, 6, 10
 ST essential protein pathogenic bacteria therapeutic target; sequence
 essential protein gene pathogenic bacteria; **mass**
spectrometry essential **protein** pathogenic
 bacteria; NMR **spectrometry** essential **protein**
 pathogenic bacteria; xray crystallog essential protein pathogenic
 bacteria; cloning essential protein pathogenic bacteria
 IT Antibacterial agents
 Cryoprotectants
 Crystallization
 DNA sequences
 Drug design
 Drug screening
 Drug targets
 Epitopes
 Escherichia coli
 Helicobacter pylori
Mass spectrometry
 Molecular cloning
 NMR spectroscopy
 Pathogenic bacteria
 Protein sequences

- Staphylococcus aureus
(cloning and phys. characterization of microbial
polypeptides involved in cellular transport and metab.
and their use as antimicrobial targets)
- IT Hydrocarbon oils
Polyoxyalkylenes, uses
(cryoprotectant; cloning and phys. characterization of microbial
polypeptides involved in cellular transport and metab.
and their use as antimicrobial targets)
- IT Solvents
(**deuterium** lock, for NMR spectroscopy; cloning and
phys. characterization of microbial **polypeptides**
involved in cellular transport and metab. and their use as
antimicrobial targets)
- IT Fusion proteins (chimeric proteins)
(for improved soly. or stability; cloning and phys.
characterization of microbial **polypeptides** involved in
cellular transport and metab. and their use as antimicrobial
targets)
- IT Elements
(heavy, for **mass spectrometry**; cloning and
phys. characterization of microbial **polypeptides**
involved in cellular transport and metab. and their use as
antimicrobial targets)
- IT Proteins
(in cellular transport and metab.; cloning and phys.
characterization of microbial **polypeptides** involved in
cellular transport and metab. and their use as antimicrobial
targets)
- IT Molecular association
(protein-protein; cloning and phys. characterization of microbial
polypeptides involved in cellular transport and metab.
and their use as antimicrobial targets)
- IT Biological transport
Metabolism, microbial
(proteins involved in; cloning and phys. characterization of
microbial **polypeptides** involved in cellular transport
and metab. and their use as antimicrobial targets)
- IT Crystallography
(x-ray; cloning and phys. characterization of microbial
polypeptides involved in cellular transport and metab.
and their use as antimicrobial targets)
- IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses
7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses
7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses
12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4,
Carbon-13, uses
(NMR **isotope**; cloning and phys. characterization of

microbial **polypeptides** involved in cellular transport
and metab. and their use as antimicrobial targets)

IT 612854-30-5P 612854-32-7P 612854-34-9P 612854-36-1P
612854-38-3P 612854-40-7P 612854-42-9P 612854-44-1P
612854-46-3P 612854-48-5P

(amino acid sequence; cloning and phys. characterization of
microbial **polypeptides** involved in cellular transport
and metab. and their use as antimicrobial targets)

IT 9013-02-9P, Adenylate kinase 9023-06-7P, UDP-acetylglucosamine
pyrophosphorylase 37251-08-4P, Enoyl-(acyl carrier protein)
reductase 50812-36-7P, Farnesyl diphosphate synthase

(cloning and phys. characterization of microbial

polypeptides involved in cellular transport and metab.
and their use as antimicrobial targets)

IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0,
Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene
glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3,

Polyethylene glycol

(cryoprotectant; cloning and phys. characterization of microbial

polypeptides involved in cellular transport and metab.
and their use as antimicrobial targets)

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 917-96-4,
Methyl-d3 isocyanide 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12 2037-
26-5 2206-27-1, Dimethyl sulfoxide-d6
2679-89-2, Diethyl-d10 ether 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6,
Dimethyl-d6 ether

(deuterium lock solvent for NMR spectroscopy; cloning
and phys. characterization of microbial **polypeptides**

involved in cellular transport and metab. and their use as
antimicrobial targets)

IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9,
Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses
7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7,
Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium,
uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses
7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses
7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9,
Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium,
uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses
7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4,
Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses
7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1,
Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses

- 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses (heavy atom for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in cellular transport and metab. and their use as antimicrobial targets)
- IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs. (mass spectrometry of; cloning and phys. characterization of microbial **polypeptides** involved in cellular transport and metab. and their use as antimicrobial targets)
- IT 612854-29-2, DNA (Staphylococcus aureus gene adk) 612854-31-6, DNA (Staphylococcus aureus gene adk) 612854-33-8, DNA (Helicobacter pylori gene glmU) 612854-35-0, DNA (Helicobacter pylori gene glmU) 612854-37-2, DNA (Escherichia coli gene ispA) 612854-39-4, DNA (Escherichia coli gene ispA) 612854-41-8, DNA (Helicobacter pylori gene fabI) 612854-43-0, DNA (Helicobacter pylori gene fabI) 612854-45-2, DNA (Helicobacter pylori gene nrdB) 612854-47-4, DNA (Helicobacter pylori gene nrdB) (nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in cellular transport and metab. and their use as antimicrobial targets)
- IT 3211-76-5, Selenomethionine (protein label for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in cellular transport and metab. and their use as antimicrobial targets)
- IT 612880-14-5 612880-15-6 612880-16-7 612880-17-8 612880-20-3 612880-21-4 612880-22-5 612880-23-6 612880-25-8 612880-26-9 (unclaimed nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in cellular transport and metab. and their use as antimicrobial targets)
- IT 612880-18-9 612880-19-0 612880-24-7 (unclaimed protein sequence; cloning and phys. characterization of microbial **polypeptides** involved in cellular transport and metab. and their use as antimicrobial targets)
- IT 612805-49-9 612805-50-2 612805-51-3 612805-52-4 612805-53-5 612805-54-6 612805-55-7 612805-56-8 612805-57-9 612805-58-0 612805-59-1 612805-60-4 (unclaimed sequence; cloning and phys. characterization of microbial **polypeptides** involved in cellular transport and metab. and their use as antimicrobial targets)
- IT 9047-64-7P, Ribonucleoside diphosphate reductase (.beta. subunit; cloning and phys. characterization of microbial

polypeptides involved in cellular transport and metab.
and their use as antimicrobial targets)

L101 ANSWER 5 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319349 Cloning and physical characterization of microbial
polypeptides involved in quorum sensing and their use as
antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi,
Masoud; Mcdonald, Merry-lynn; Li, Qin; Awrey, Donald; Beattie, Bryan
(Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO
2003087145 A2 20031023, 179 pp. DESIGNATED STATES: W: AE, AG, AL,
AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ,
DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD,
MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD,
SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU,
ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ,
CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU,
MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN:
PIXXD2. APPLICATION: WO 2003-CA483 20030408. PRIORITY: US
2002-PV370806 20020408; US 2002-PV370978 20020409; US 2002-PV371009
20020409.

AB The present invention relates to **polypeptide** targets for
pathogenic bacteria. Reliable, high throughput methods are
developed to identify, express, and purify a no. of antimicrobial
targets from Escherichia coli and Pseudomonas aeruginosa. The
nucleic acid and amino acid sequences are provided for RhlR and LasR
homolog, autoinducer synthesis protein RhlI, and autoinducer
synthesis protein LasI. The invention also provides bioinformatic,
biochem. and biophys. characteristics of those **polypeptides**
, in particular characterization by **mass**
spectrometry, **NMR spectrometry**, and x-ray
crystallog.

IT 7782-39-0, Hydrogen-2, uses
(NMR **isotope**; cloning and phys. characterization of
microbial **polypeptides** involved in quorum sensing and
their use as antimicrobial targets)

RN 7782-39-0 HCA
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

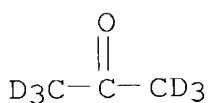
D-D

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 917-96-4,
Methyl-d3 isocyanide 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
2037-26-5 2206-27-1, Dimethyl sulfoxide-d6

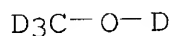
2679-89-2, Diethyl-d10 ether 4472-41-7,
 N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
 7789-20-0, Deuterium oxide 17222-37-6,
 Dimethyl-d6 ether

(deuterium lock solvent for NMR spectroscopy; cloning
 and phys. characterization of microbial **polypeptides**
 involved in quorum sensing and their use as antimicrobial
 targets)

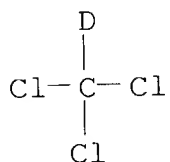
RN 666-52-4 HCA
 CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



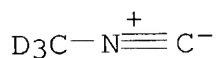
RN 811-98-3 HCA
 CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



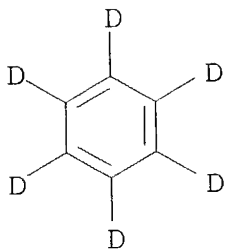
RN 865-49-6 HCA
 CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



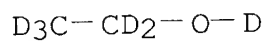
RN 917-96-4 HCA
 CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



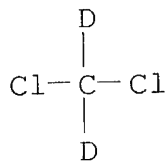
RN 1076-43-3 HCA
 CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



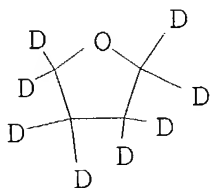
RN 1516-08-1 HCA
 CN Ethanol-d6 (9CI) (CA INDEX NAME)



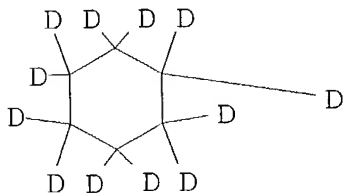
RN 1665-00-5 HCA
 CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



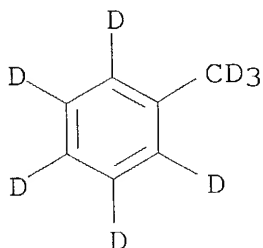
RN 1693-74-9 HCA
 CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



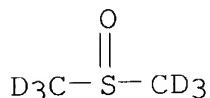
RN 1735-17-7 HCA
 CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



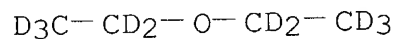
RN 2037-26-5 HCA
CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



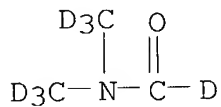
RN 2206-27-1 HCA
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



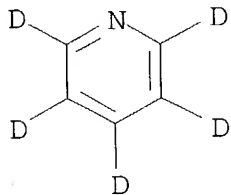
RN 2679-89-2 HCA
CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 4472-41-7 HCA
CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7291-22-7 HCA
CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA

CN Water-d2 (9CI) (CA INDEX NAME)

D-O-D

RN 17222-37-6 HCA

CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)

D3C-O-CD3

IC ICM C07K014-245

ICS C12N015-31; C12N015-62; G01N033-50; C07K014-21

CC 7-2 (Enzymes)

Section cross-reference(s): 1, 3, 6, 10

ST essential protein pathogenic bacteria therapeutic target; sequence
essential protein gene pathogenic bacteria; **mass**
spectrometry essential **protein** pathogenic
bacteria; NMR **spectrometry** essential **protein**
pathogenic bacteria; xray crystallog essential protein pathogenic
bacteria; cloning essential protein pathogenic bacteria

IT Proteins

(RhIR and LasR homolog; cloning and phys. characterization of
microbial **polypeptides** involved in quorum sensing and
their use as antimicrobial targets)

IT Proteins

(autoinducer synthesis LasI; cloning and phys. characterization
of microbial **polypeptides** involved in quorum sensing
and their use as antimicrobial targets)

IT Proteins

(autoinducer synthesis RhII; cloning and phys. characterization
of microbial **polypeptides** involved in quorum sensing
and their use as antimicrobial targets)

IT Antibacterial agents

Cryoprotectants

Crystallization

DNA sequences

Drug design

Drug screening

Drug targets

Epitopes

Escherichia coli

Mass spectrometry

Molecular cloning

NMR spectroscopy

Pathogenic bacteria

Protein sequences

Pseudomonas aeruginosa

(cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT Hydrocarbon oils

Polyoxyalkylenes, uses

(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT Solvents

(**deuterium** lock, for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT Fusion proteins (chimeric proteins)

(for improved soly. or stability; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT Elements

(heavy, for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT **Proteins**

(in quorum **sensing**; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT Molecular association

(protein-protein; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT Quorum **sensing**

(**proteins** involved in; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT Crystallography

(x-ray; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses

(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

IT 612554-26-4P, Protein (Escherichia coli gene sdiA) 612554-28-6P
612554-30-0P 612554-32-2P 612554-34-4P

(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

- IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0, Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3, **Polyethylene glycol**

(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

- IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6, Chloroform-d 917-96-4, Methyl-d3 isocyanide 1076-43-3, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6 2679-89-2, Diethyl-d10 ether 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, **Deuterium** oxide 17222-37-6, Dimethyl-d6 ether

(**deuterium** lock solvent for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

- IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9, Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses 7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7, Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium, uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses 7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses 7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9, Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium, uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses 7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4, Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses 7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1, Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses

(heavy atom for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

- IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs.

(**mass spectrometry** of; cloning and phys.

- characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)
- IT 612554-25-3, DNA (Escherichia coli gene sdiA) 612554-27-5, DNA (Pseudomonas aeruginosa gene rhlI) 612554-29-7, DNA (Pseudomonas aeruginosa gene rhlI) 612554-31-1, DNA (Pseudomonas aeruginosa gene lasI) 612554-33-3, DNA (Pseudomonas aeruginosa gene lasI) (nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)
- IT 3211-76-5, Selenomethionine (protein label for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)
- IT 612574-07-9 612574-08-0 612574-10-4 612574-11-5 612574-12-6 612574-13-7 (unclaimed nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)
- IT 612574-09-1 (unclaimed protein sequence; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)
- IT 612507-63-8 612507-65-0 612507-69-4 612507-73-0 612507-78-5 612507-85-4 612507-90-1 612507-96-7 (unclaimed sequence; cloning and phys. characterization of microbial **polypeptides** involved in quorum sensing and their use as antimicrobial targets)

L101 ANSWER 6 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319345 Cloning and physical characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Domagala, Megan; Kanagarajah, Dhushy; Awrey, Donald; Beattie, Bryan; McDonald, Merry-Lynn; Nethery, Kathleen; Mansoury, Kamran; Ouyang, Hui (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003085103 A2 20031016, 212 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-CA472 20030404. PRIORITY: US 2002-PV369822 20020404; US 2002-PV370849 20020408; US 2002-PV370854 20020408; US 2002-PV370860 20020408; US 2002-PV371066 20020409; US

2002-PV371151 20020409.

AB The present invention relates to **polypeptide** targets for pathogenic bacteria. Reliable, high throughput methods are developed to identify, express, and purify a no. of antimicrobial targets from Staphylococcus aureus, Escherichia coli, Streptococcus pneumoniae, and Pseudomonas aeruginosa. The nucleic acid and amino acid sequences are provided for cell division protein FtsA, GTP-binding protein Era, cell division protein FtsZ, and the gene yihA conserved hypothetical protein from Escherichia coli and Pseudomonas aeruginosa. The invention also provides bioinformatic, biochem. and biophys. characteristics of those **polypeptides**, in particular characterization by **mass spectrometry**, **NMR spectrometry**, and x-ray crystallog.

IT 7782-39-0, Hydrogen-2, uses
(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)

RN 7782-39-0 HCA

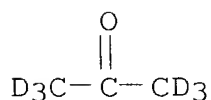
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 917-96-4,
Methyl-d3 isocyanide 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
2037-26-5 2206-27-1, Dimethyl sulfoxide-d6
2679-89-2, Diethyl-d10 ether 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6,
Dimethyl-d6 ether
(**deuterium** lock solvent for NMR spectroscopy; cloning
and phys. characterization of microbial **polypeptides**
involved in nucleotide hydrolysis and their use as antimicrobial
targets)

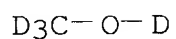
RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



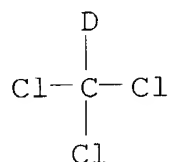
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



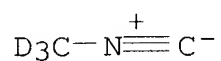
RN 865-49-6 HCA

CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



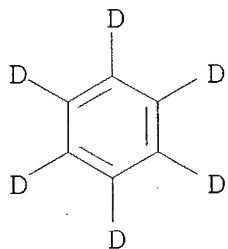
RN 917-96-4 HCA

CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



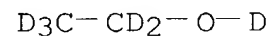
RN 1076-43-3 HCA

CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



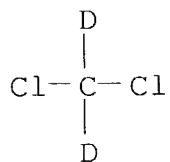
RN 1516-08-1 HCA

CN Ethanol-d6 (9CI) (CA INDEX NAME)

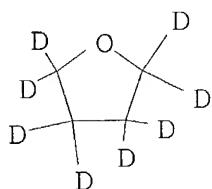


RN 1665-00-5 HCA

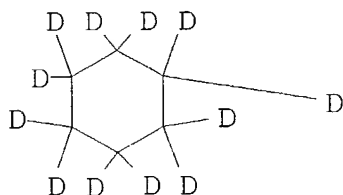
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



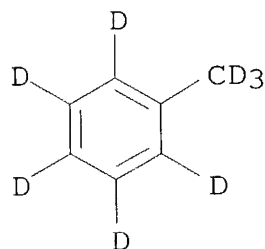
RN 1693-74-9 HCA
CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



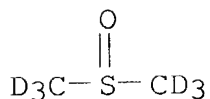
RN 1735-17-7 HCA
CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



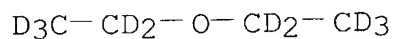
RN 2037-26-5 HCA
CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



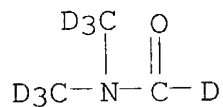
RN 2206-27-1 HCA
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



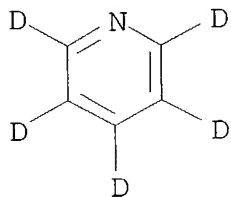
RN 2679-89-2 HCA
CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



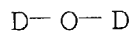
RN 4472-41-7 HCA
CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



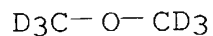
RN 7291-22-7 HCA
CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IC ICM C12N009-10

ICS G06F017-50

CC 7-2 (Enzymes)

Section cross-reference(s): 1, 3, 6, 10

ST essential protein pathogenic bacteria therapeutic target; sequence

- essential protein gene pathogenic bacteria; **mass spectrometry** essential **protein** pathogenic bacteria; NMR **spectrometry** essential **protein** pathogenic bacteria; xray crystallog essential protein pathogenic bacteria; cloning essential protein pathogenic bacteria
- IT Molecular chaperones
(DnaK, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Proteins
(GTP-binding, gene Era; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Heat-shock proteins
(HSP 70, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(L13, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(L14, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(L2, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(L5, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(S11, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(S19, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(S7, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Ribosomal proteins
(S9, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in

- nucleotide hydrolysis and their use as antimicrobial targets)
- IT Antibacterial agents
Cryoprotectants
Crystallization
DNA sequences
Drug design
Drug screening
Drug targets
Epitopes
Escherichia coli
 Mass spectrometry
Molecular cloning
NMR spectroscopy
Pathogenic bacteria
Protein sequences
Pseudomonas aeruginosa
Staphylococcus aureus
Streptococcus pneumoniae
 (cloning and phys. characterization of microbial
 polypeptides involved in nucleotide hydrolysis and their
 use as antimicrobial targets)
- IT Hydrocarbon oils
 Polyoxyalkylenes, uses
 (cryoprotectant; cloning and phys. characterization of microbial
 polypeptides involved in nucleotide hydrolysis and their
 use as antimicrobial targets)
- IT Solvents
 (**deuterium** lock, for NMR spectroscopy; cloning and
 phys. characterization of microbial **polypeptides**
 involved in nucleotide hydrolysis and their use as antimicrobial
 targets)
- IT Fusion proteins (chimeric proteins)
 (for improved soly. or stability; cloning and phys.
 characterization of microbial **polypeptides** involved in
 nucleotide hydrolysis and their use as antimicrobial targets)
- IT Proteins
 (ftsA; cloning and phys. characterization of microbial
 polypeptides involved in nucleotide hydrolysis and their
 use as antimicrobial targets)
- IT Proteins
 (ftsZ; cloning and phys. characterization of microbial
 polypeptides involved in nucleotide hydrolysis and their
 use as antimicrobial targets)
- IT Proteins
 (gene yihA; cloning and phys. characterization of microbial
 polypeptides involved in nucleotide hydrolysis and their
 use as antimicrobial targets)
- IT Elements

(heavy, for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)

- IT Proteins
(in nucleotide hydrolysis; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Molecular association
(protein-protein; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Nucleotides, biological studies
(proteins involved in hydrolysis of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT Crystallography
(x-ray; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses **7782-39-0**, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses
(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT 612853-29-9P 612853-31-3P 612853-33-5P 612853-35-7P
612853-37-9P 612853-39-1P 612853-41-5P, Protein (Escherichia coli gene yihA) 612853-43-7P, Protein (Escherichia coli gene yihA)
612853-45-9P 612853-48-2P 612853-50-6P
(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0, Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3,
Polyethylene glycol
(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT **666-52-4**, 2-Propanone-1,1,1,3,3,3-d6 **811-98-3**, Methanol-d4 **865-49-6**, Chloroform-d **917-96-4**, Methyl-d3 isocyanide **1076-43-3**, Benzene-d6 **1516-08-1**, Ethanol-d6 **1665-00-5** **1693-74-9**, Tetrahydrofuran-d8 **1735-17-7**, Cyclohexane-d12 **2037-26-5** **2206-27-1**, Dimethyl sulfoxide-d6

2679-89-2, Diethyl-d10 ether 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6,
Dimethyl-d6 ether

(deuterium lock solvent for NMR spectroscopy; cloning
and phys. characterization of microbial **polypeptides**
involved in nucleotide hydrolysis and their use as antimicrobial
targets)

IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9,
Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses
7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7,
Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium,
uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses
7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses
7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9,
Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium,
uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses
7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4,
Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses
7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1,
Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses
7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5,
Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses
7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2,
Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses
(heavy atom for **mass spectrometry**; cloning
and phys. characterization of microbial **polypeptides**
involved in nucleotide hydrolysis and their use as antimicrobial
targets)

IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid,
derivs.

(**mass spectrometry** of; cloning and phys.
characterization of microbial **polypeptides** involved in
nucleotide hydrolysis and their use as antimicrobial targets)

IT 612853-28-8, DNA (Streptococcus pneumoniae gene ftsA) 612853-30-2,
DNA (Streptococcus pneumoniae gene ftsA) 612853-32-4, DNA
(Staphylococcus aureus gene era) 612853-34-6, DNA (Staphylococcus
aureus gene era) 612853-36-8, DNA (Streptococcus pneumoniae gene
ftsZ) 612853-38-0, DNA (Streptococcus pneumoniae gene ftsZ)
612853-40-4, DNA (Escherichia coli gene yihA) 612853-42-6, DNA
(Escherichia coli gene yihA) 612853-44-8, DNA (Pseudomonas
aeruginosa gene yihA) 612853-46-0, DNA (Pseudomonas aeruginosa
gene yihA) 612853-47-1, DNA (Streptococcus pneumoniae gene era)
612853-49-3, DNA (Streptococcus pneumoniae gene era)

(nucleotide sequence; cloning and phys. characterization of
microbial **polypeptides** involved in nucleotide
hydrolysis and their use as antimicrobial targets)

IT 3211-76-5, Selenomethionine

(protein label for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)

- IT 9014-08-8, Enolase 9055-66-7, Phenylalanyl-tRNA synthetase
9068-08-0, Formate acetyltransferase
(protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT 612865-89-1 612865-90-4 612865-92-6 612865-93-7 612865-95-9
612865-96-0 612865-97-1 612865-98-2 612865-99-3 612866-00-9
612866-01-0 612866-02-1
(unclaimed nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT 612865-91-5 612865-94-8
(unclaimed protein sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)
- IT 612817-60-4 612817-61-5 612817-62-6 612817-63-7 612817-64-8
612817-65-9 612817-66-0 612817-67-1 612817-68-2 612817-69-3
612817-70-6 612817-71-7 612817-72-8 612817-73-9 612817-74-0
612817-75-1
(unclaimed sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleotide hydrolysis and their use as antimicrobial targets)

L101 ANSWER 7 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319344 Cloning and physical characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Domagala, Megan; Nethery, Kathleen; Awrey, Donald; Beattie, Bryan; Mcdonald, Merry-Lynn; Houston, Simon; Arrowsmith, Cheryl; Mansoury, Kamran; Ouyang, Hui; Kanagarajah, Dhushy; Ng, Ivy; Vallee, Francois (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003084987 A2 20031016, 289 pp.
DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-CA465 20030404. PRIORITY: US 2002-PV370060 20020404; US 2002-PV369831 20020404; US 2002-PV369819 20020404; US 2002-PV369826 20020404; US 2002-PV370852 20020408; US 2002-PV370681 20020408; US 2002-PV371014

20020409; US 2002-PV371180 20020409; US 2002-PV371008 20020409; US 2002-PV371114 20020409; US 2002-PV371189 20020409; US 2002-PV371064 20020409.

AB The present invention relates to **polypeptide** targets for pathogenic bacteria. Reliable, high throughput methods are developed to identify, express, and purify a no. of antimicrobial targets from Staphylococcus aureus, Escherichia coli, Streptococcus pneumoniae, Helicobacter pylori, and Pseudomonas aeruginosa. The nucleic acid and amino acid sequences are provided for GroES protein, transcription termination factor NusG, GrpE protein, RNA polymerase .alpha. subunit, prolyl-tRNA synthetase, seryl-tRNA synthetase, and L-Cysteine desulfurase. The invention also provides bioinformatic, biochem. and biophys. characteristics of those **polypeptides**, in particular characterization by **mass spectrometry**, **NMR spectrometry**, and x-ray crystallog.

IT 7782-39-0, Hydrogen-2, uses
(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)

RN 7782-39-0 HCA

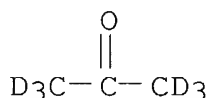
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

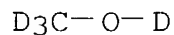
IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6, Chloroform-d 917-96-4, Methyl-d3 isocyanide 1076-43-3, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6 2679-89-2, Diethyl-d10 ether 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, **Deuterium** oxide 17222-37-6, Dimethyl-d6 ether
(**deuterium** lock solvent for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)

RN 666-52-4 HCA

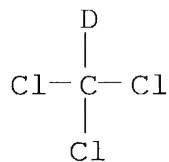
CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



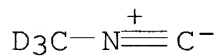
RN 811-98-3 HCA
CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



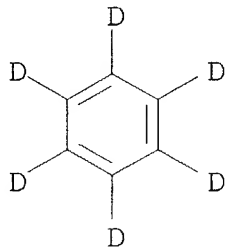
RN 865-49-6 HCA
CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



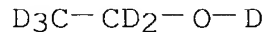
RN 917-96-4 HCA
CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



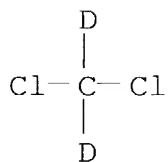
RN 1076-43-3 HCA
CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



RN 1516-08-1 HCA
CN Ethanol-d6 (9CI) (CA INDEX NAME)

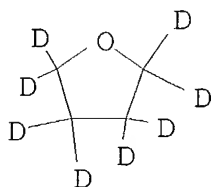


RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



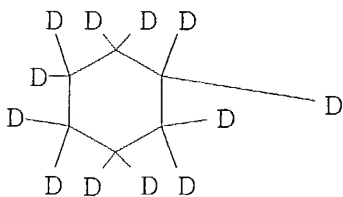
RN 1693-74-9 HCA

CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



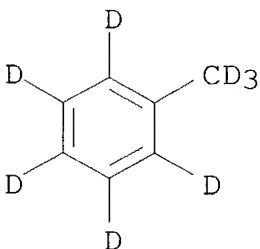
RN 1735-17-7 HCA

CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



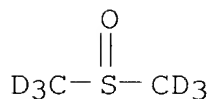
RN 2037-26-5 HCA

CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)

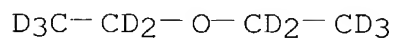


RN 2206-27-1 HCA

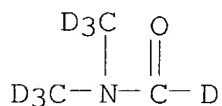
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



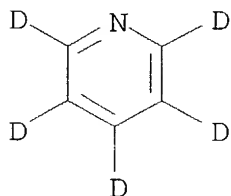
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



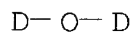
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



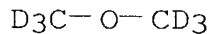
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IC ICM C07K014-00
 CC 7-2 (Enzymes)
 Section cross-reference(s): 1, 3, 6, 10
 ST essential protein pathogenic bacteria therapeutic target; sequence
 essential protein gene pathogenic bacteria; **mass**

- spectrometry** essential **protein** pathogenic bacteria; NMR **spectrometry** essential **protein** pathogenic bacteria; xray crystallog essential protein pathogenic bacteria; cloning essential protein pathogenic bacteria
- IT Molecular chaperones
(DnaK, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Molecular chaperones
(GroES; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Proteins
(GrpE; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Heat-shock proteins
(HSP 70, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Ribosomal proteins
(L1, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Antibacterial agents
Cryoprotectants
Crystallization
DNA sequences
Drug design
Drug screening
Drug targets
Epitopes
Escherichia coli
Helicobacter pylori
Mass spectrometry
Molecular cloning
NMR spectroscopy
Pathogenic bacteria
Protein sequences
Pseudomonas aeruginosa
Staphylococcus aureus
Streptococcus pneumoniae
(cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)

- IT Hydrocarbon oils
Polyoxyalkylenes, uses
(cryoprotectant; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Solvents
(deuterium lock, for NMR spectroscopy; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Fusion proteins (chimeric proteins)
(for improved soly. or stability; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Transcription factors
(gene nusG; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Elements
(heavy, for mass spectrometry; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Proteins
(in nucleic acid synthesis and processing; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Molecular association
(protein-protein; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Crystallography
(x-ray; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT Transcription factors
(.rho., protein-protein interactions of; cloning and phys. characterization of microbial polypeptides involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses
(NMR isotope; cloning and phys. characterization of

- microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 612813-91-9 612866-19-0 612866-20-3
(Unclaimed; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 612853-52-8P 612853-54-0P 612853-56-2P 612853-58-4P
612853-60-8P 612853-62-0P 612853-64-2P 612853-66-4P
612853-68-6P 612853-70-0P 612853-72-2P 612853-74-4P
612853-76-6P 612853-79-9P 612853-81-3P 612853-83-5P
612853-85-7P 612853-87-9P 612853-89-1P
(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 9023-48-7P, Seryl-tRNA synthetase 9055-68-9P, Prolyl-tRNA synthetase 149371-08-4P, **Cysteine** desulfurase
(cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0, Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3, **Polyethylene glycol**
(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6, Chloroform-d 917-96-4, Methyl-d3 isocyanide 1076-43-3, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6 2679-89-2, Diethyl-d10 ether 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, **Deuterium** oxide 17222-37-6, Dimethyl-d6 ether
(**deuterium** lock solvent for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 9073-60-3, Metallo-.beta.-lactamase
(family member, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9, Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses 7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7,

- Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium, uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses 7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses 7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9, Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium, uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses 7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4, Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses 7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1, Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses (heavy atom for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs.
(**mass spectrometry** of; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 612853-51-7, DNA (Staphylococcus aureus gene groES) 612853-53-9, DNA (Pseudomonas aeruginosa gene groES) 612853-55-1, DNA (Helicobacter pylori gene groES) 612853-57-3, DNA (Escherichia coli gene nusG) 612853-59-5, DNA (Staphylococcus aureus gene grpE) 612853-61-9, DNA (Staphylococcus aureus gene grpE) 612853-63-1, DNA (Helicobacter pylori gene nusG) 612853-65-3, DNA (Helicobacter pylori gene nusG) 612853-67-5 612853-69-7 612853-71-1, DNA (Helicobacter pylori gene rpoA) 612853-73-3, DNA (Helicobacter pylori gene rpoA) 612853-75-5, DNA (Staphylococcus aureus gene rpoA) 612853-77-7, DNA (Staphylococcus aureus gene rpoA) 612853-78-8, DNA (Helicobacter pylori gene proS) 612853-80-2, DNA (Helicobacter pylori gene proS) 612853-82-4, DNA (Streptococcus pneumoniae gene serS) 612853-84-6, DNA (Streptococcus pneumoniae gene serS) 612853-86-8, DNA (Pseudomonas aeruginosa gene iscS) 612853-88-0, DNA (Pseudomonas aeruginosa gene iscS)
(nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 3211-76-5, Selenomethionine
(protein label for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)
- IT 9012-90-2, DNA polymerase

(protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)

IT 612866-21-4 612866-22-5 612866-24-7 612866-25-8 612866-26-9
612866-27-0 612866-28-1 612866-29-2 612866-30-5 612866-31-6

(unclaimed nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)

IT 612813-58-8 612813-60-2 612813-62-4 612813-63-5 612813-64-6
612813-67-9 612813-69-1 612813-71-5 612813-73-7 612813-75-9
612813-77-1 612813-79-3 612813-81-7 612813-83-9 612813-85-1
612813-87-3 612813-89-5 612813-93-1 612813-95-3 612813-97-5
612813-99-7 612814-01-4 612814-03-6 612814-05-8 612814-07-0
612814-09-2 612814-11-6 612814-13-8 612814-15-0 612814-17-2
612814-19-4 612814-21-8 612814-23-0 612866-03-2 612866-04-3
612866-05-4 612866-06-5 612866-07-6 612866-08-7 612866-09-8
612866-10-1 612866-12-3 612866-13-4 612866-14-5 612866-15-6
612866-16-7 612866-17-8 612866-18-9 612866-23-6

(unclaimed sequence; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)

IT 9014-24-8P, RNA polymerase
(.alpha. subunit; cloning and phys. characterization of microbial **polypeptides** involved in nucleic acid synthesis and processing and their use as antimicrobial targets)

L101 ANSWER 8 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319343 Cloning and physical characterization of microbial **polypeptides** involved in cellular metabolism and their use as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Domagala, Megan; Kanagarajah, Dhushy; Ouyang, Hui; Houston, Simon; Awrey, Donald; Beattie, Bryan; Nethery, Kathleen; Mansoury, Kamran; Buzadzija, Kristina; Ng, Ivy; Mcdonald, Merry-lynn; Richards, Dawn; Thalakada, Rosanne; Virag, Cristina; Alam, Muhammad Zahoor; Canadien, Veronica (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003084986 A2 20031016, 285 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-CA464 20030404. PRIORITY: US 2002-PV369817 20020404; US 2002-PV370102 20020404; US

2002-PV370820 20020408; US 2002-PV370859 20020408; US 2002-PV370778 20020408; US 2002-PV370792 20020408; US 2002-PV371140 20020409; US 2002-PV386018 20020605; US 2002-PV386430 20020606; US 2002-PV436842 20021227; US 2002-PV436987 20021230.

AB The present invention relates to **polypeptide** targets for pathogenic bacteria. Reliable, high throughput methods are developed to identify, express, and purify a no. of antimicrobial targets from *Staphylococcus aureus*, *Escherichia coli*, *Streptococcus pneumoniae*, *Haemophilus influenzae*, and *Pseudomonas aeruginosa*. The nucleic acid and amino acid sequences are provided for ribulose phosphate 3-epimerase, acetyl-CoA carboxylase/transferase .beta. subunit, DNA gyrase subunit B, biotin carboxylase, riboflavin kinase/FAD synthase, phosphopantetheine adenylyltransferase, inorg. pyrophosphatase, and phosphoglucosamine mutase. The invention also provides bioinformatic, biochem. and biophys. characteristics of those **polypeptides**, in particular characterization by **mass spectrometry**, **NMR spectrometry**, and x-ray crystallog.

IT 7782-39-0, Hydrogen-2, uses
(**NMR isotope**; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)

RN 7782-39-0 HCA

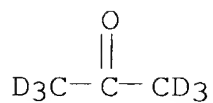
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

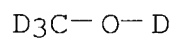
IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 917-96-4,
Methyl-d3 isocyanide 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
2037-26-5 2206-27-1, Dimethyl sulfoxide-d6
2679-89-2, Diethyl-d10 ether 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6,
Dimethyl-d6 ether
(**deuterium** lock solvent for NMR spectroscopy; cloning
and phys. characterization of microbial **polypeptides**
involved in cellular metab. and their use as antimicrobial
targets)

RN 666-52-4 HCA

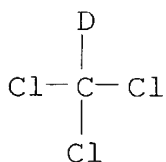
CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



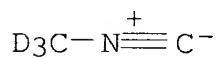
RN 811-98-3 HCA
 CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



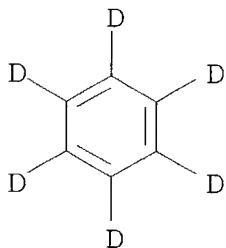
RN 865-49-6 HCA
 CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



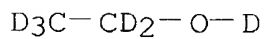
RN 917-96-4 HCA
 CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



RN 1076-43-3 HCA
 CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)

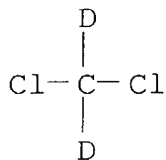


RN 1516-08-1 HCA
 CN Ethanol-d6 (9CI) (CA INDEX NAME)



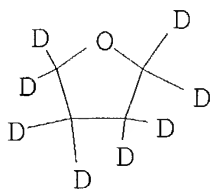
RN 1665-00-5 HCA

CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



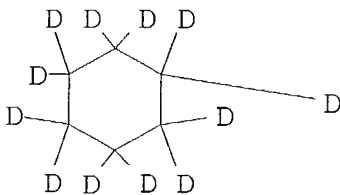
RN 1693-74-9 HCA

CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



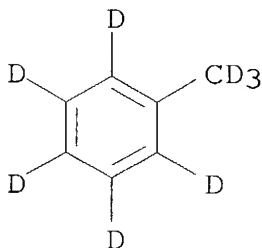
RN 1735-17-7 HCA

CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



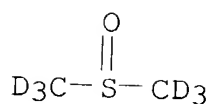
RN 2037-26-5 HCA

CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)

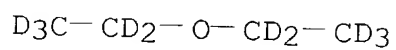


RN 2206-27-1 HCA

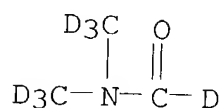
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



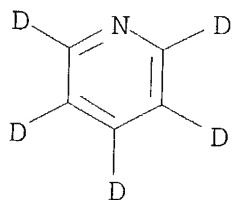
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



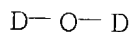
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



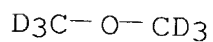
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IC ICM C07K014-00
 CC 7-2 (Enzymes)

ST Section cross-reference(s): 1, 3, 6, 10
 essential protein pathogenic bacteria therapeutic target; sequence
 essential protein gene pathogenic bacteria; mass
 spectrometry essential protein pathogenic

- bacteria; NMR **spectrometry** essential **protein**
pathogenic bacteria; xray crystallog essential protein pathogenic
bacteria; cloning essential protein pathogenic bacteria
- IT Molecular chaperones
(60-kilodalton, protein-protein interactions of; cloning and
phys. characterization of microbial **polypeptides**
involved in cellular metab. and their use as antimicrobial
targets)
- IT Enzymes, biological studies
(DNA gyrases, subunit B; cloning and phys. characterization of
microbial **polypeptides** involved in cellular metab. and
their use as antimicrobial targets)
- IT Molecular chaperones
(DnaK, protein-protein interactions of; cloning and phys.
characterization of microbial **polypeptides** involved in
cellular metab. and their use as antimicrobial targets)
- IT Proteins
(GrpE, protein-protein interactions of; cloning and phys.
characterization of microbial **polypeptides** involved in
cellular metab. and their use as antimicrobial targets)
- IT Antibacterial agents
Cryoprotectants
Crystallization
DNA sequences
Drug design
Drug screening
Drug targets
Enterococcus faecalis
Epitopes
Escherichia coli
Haemophilus influenzae
Mass spectrometry
Molecular cloning
NMR spectroscopy
Pathogenic bacteria
Protein sequences
Pseudomonas aeruginosa
Staphylococcus aureus
Streptococcus pneumoniae
(cloning and phys. characterization of microbial
polypeptides involved in cellular metab. and their use as
antimicrobial targets)
- IT Hydrocarbon oils
Polyoxyalkylenes, uses
(cryoprotectant; cloning and phys. characterization of microbial
polypeptides involved in cellular metab. and their use as
antimicrobial targets)
- IT Solvents

(deuterium lock, for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)

- IT Fusion proteins (chimeric proteins)
(for improved soly. or stability; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT Flagellins
(gene fliC, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT Elements
(heavy, for mass spectrometry; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT Proteins
(in cellular metab.; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT Molecular association
(protein-protein; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT Metabolism, microbial
(proteins involved in; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT Crystallography
(x-ray; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses
(NMR isotope; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 612853-91-5P 612853-93-7P 612853-95-9P 612853-97-1P
612854-00-9P 612854-02-1P 612854-04-3P 612854-06-5P
612854-08-7P 612854-11-2P 612854-13-4P 612854-15-6P
612854-17-8P 612854-19-0P 612854-21-4P 612854-23-6P
612854-26-9P 612854-28-1P
(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and

- their use as antimicrobial targets)
- IT 9000-83-3, ATPase
(cation-transporting, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 9024-20-8P, Ribulose phosphate 3-epimerase 9024-82-2P, Inorg. pyrophosphatase 9026-37-3P, FAD synthetase 9026-99-7P, Phosphopantetheine adenylyltransferase 9031-92-9P, Phosphoglucosamine mutase 9032-82-0P, Riboflavin kinase 9075-71-2P, Biotin carboxylase
(cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0, Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3, **Polyethylene glycol**
(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6, Chloroform-d 917-96-4, Methyl-d3 isocyanide 1076-43-3, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6 2679-89-2, Diethyl-d10 ether 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, Deuterium oxide 17222-37-6, Dimethyl-d6 ether
(deuterium lock solvent for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9, Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses 7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7, Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium, uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses 7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses 7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9, Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium, uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses 7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4, Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses 7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1, Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses

- 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses (heavy atom for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs. (mass spectrometry of; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 612853-90-4, DNA (Staphylococcus aureus gene rpe) 612853-92-6, DNA (Escherichia coli gene rpe) 612853-94-8, DNA (Escherichia coli gene rpe) 612853-96-0, DNA (Staphylococcus aureus gene accD) 612853-98-2, DNA (Staphylococcus aureus gene accD) 612853-99-3, DNA (Streptococcus pneumoniae gene gyrB) 612854-01-0, DNA (Streptococcus pneumoniae gene gyrB) 612854-03-2, DNA (Staphylococcus aureus gene accC) 612854-05-4, DNA (Staphylococcus aureus gene accC) 612854-07-6, DNA (Pseudomonas aeruginosa gene accC) 612854-09-8, DNA (Pseudomonas aeruginosa gene accC) 612854-10-1, DNA (Pseudomonas aeruginosa gene rpe) 612854-12-3, DNA (Pseudomonas aeruginosa gene rpe) 612854-14-5, DNA (Streptococcus pneumoniae gene ribC) 612854-16-7, DNA (Streptococcus pneumoniae gene ribC) 612854-18-9, DNA (Streptococcus pneumoniae gene kdtB) 612854-20-3, DNA (Streptococcus pneumoniae gene kdtB) 612854-22-5, DNA (Haemophilus influenzae gene IPYR) 612854-24-7, DNA (Haemophilus influenzae gene IPYR) 612854-25-8, DNA (Pseudomonas aeruginosa gene MRSA) 612854-27-0, DNA (Pseudomonas aeruginosa gene MRSA) (nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 3211-76-5, Selenomethionine (protein label for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 9014-08-8, Enolase 9023-46-5, Threonyl-tRNA synthetase 71822-24-7, Malate:quinone oxidoreductase (protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)
- IT 612838-99-0 612839-00-6 612839-01-7 612839-02-8 612839-03-9
 612839-04-0 612839-05-1 612839-06-2 612839-07-3 612839-08-4
 612839-09-5 612839-10-8 612839-11-9 612839-12-0 612839-13-1
 612839-14-2 612839-15-3 612839-16-4 612839-17-5 612839-18-6

612839-19-7	612839-20-0	612839-21-1	612839-22-2	612839-23-3
612839-24-4	612839-25-5	612839-26-6	612839-27-7	612839-28-8
612839-29-9	612866-32-7	612866-33-8	612866-34-9	612866-35-0
612866-36-1	612866-37-2	612866-38-3	612866-39-4	612866-40-7
612866-41-8	612866-42-9	612866-43-0	612866-44-1	612866-45-2
612866-46-3	612866-47-4	612866-48-5	612866-49-6	612866-50-9
612866-51-0	612866-52-1	612866-53-2	612866-54-3	612866-55-4

(unclaimed sequence; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)

IT 9023-93-2P, Acetyl-CoA carboxylase
(.beta.-subunit; cloning and phys. characterization of microbial **polypeptides** involved in cellular metab. and their use as antimicrobial targets)

L101 ANSWER 9 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:319340 Cloning and physical characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad Zahoor; Arrowsmith, Cheryl; Awrey, Donald; Beattie, Bryan; Richards, Dawn; Canadien, Veronica; Domagala, Megan; Houston, Simon; Mansoury, Kamran; Li, Qin; Nethery, Kathleen; Virag, Cristina; Ng, Ivy; Ouyang, Hui; Tai, Matthew; Thalakada, Rosanne; Kanagarajah, Dhushy (Affinium Pharmaceuticals, Inc., Can.; et al.). PCT Int. Appl. WO 2003083099 A2 20031009, 369 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2003-CA462 20030402. PRIORITY: US 2002-PV369511 20020402; US 2002-PV385089 20020531; US 2002-PV385751 20020604; US 2002-PV386553 20020605; US 2002-PV386577 20020605; US 2002-PV386367 20020605; US 2002-PV386566 20020605; US 2002-PV386390 20020606; US 2002-PV386601 20020606; US 2002-PV399972 20020731; US 2002-PV424053 20021105; US 2002-PV436834 20021227; US 2002-PV436804 20021227; US 2002-PV436861 20021227; US 2002-PV437281 20021231; US 2002-PV437527 20021231.

AB The present invention relates to **polypeptide** targets for pathogenic bacteria. Reliable, high throughput methods are developed to identify, express, and purify a no. of antimicrobial targets from Staphylococcus aureus, Escherichia coli, Streptococcus pneumoniae, Enterococcus faecalis, Haemophilus influenzae, and Pseudomonas aeruginosa. The nucleic acid and amino acid sequences are provided for O-sialoglycoprotein endopeptidase, glycyl-tRNA

synthetase .alpha.-subunit, translation elongation factor G, methionine aminopeptidase, phenylalanyl-tRNA synthetase .alpha.-subunit, **peptide** chain release factor RF-2, tRNA (guanine-7-)methyltransferase, and histidyl-tRNA synthetase. The invention also provides bioinformatic, biochem. and biophys. characteristics of those **polypeptides**, in particular characterization by **mass spectrometry**, NMR **spectrometry**, and x-ray crystallog.

IT 7782-39-0, Hydrogen-2, uses
 (NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)

RN 7782-39-0 HCA

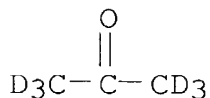
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
 Methanol-d4 865-49-6, Chloroform-d 917-96-4,
 Methyl-d3 isocyanide 1076-43-3, Benzene-d6
 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
 , Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
 2037-26-5 2206-27-1, Dimethyl sulfoxide-d6
 2679-89-2, Diethyl-d10 ether 4472-41-7,
 N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
 7789-20-0, **Deuterium** oxide 17222-37-6,
 Dimethyl-d6 ether
 (deuterium lock solvent for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)

RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



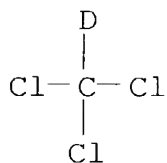
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

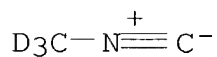
D3C-O-D

RN 865-49-6 HCA

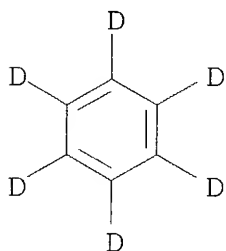
CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



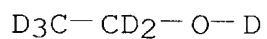
RN 917-96-4 HCA
 CN Methane-d3, isocyano- (9CI) (CA INDEX NAME)



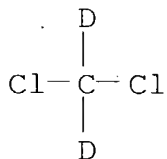
RN 1076-43-3 HCA
 CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



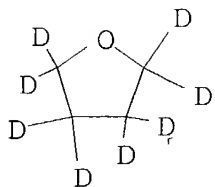
RN 1516-08-1 HCA
 CN Ethanol-d6 (9CI) (CA INDEX NAME)



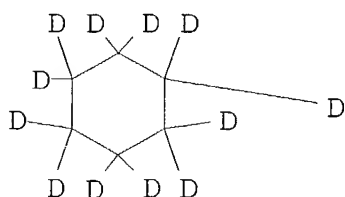
RN 1665-00-5 HCA
 CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



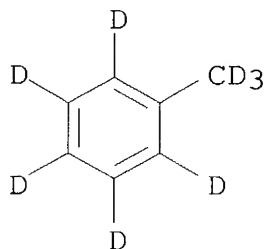
RN 1693-74-9 HCA
 CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



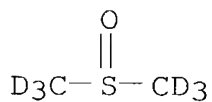
RN 1735-17-7 HCA
 CN Cyclohexane-d12 (6CI, 8CI, 9CI) (CA INDEX NAME)



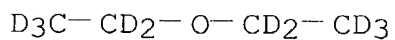
RN 2037-26-5 HCA
 CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



RN 2206-27-1 HCA
 CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)

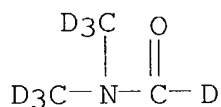


RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



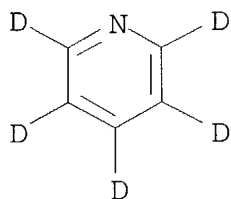
RN 4472-41-7 HCA

CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



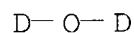
RN 7291-22-7 HCA

CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



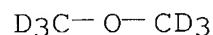
RN 7789-20-0 HCA

CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA

CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IC ICM C12N009-10

ICS G06F017-50

CC 7-2 (Enzymes)

Section cross-reference(s): 1, 3, 6, 10

ST essential protein pathogenic bacteria therapeutic target; sequence

essential protein gene pathogenic bacteria; **mass**

spectrometry essential **protein** pathogenic

bacteria; NMR **spectrometry** essential **protein**

pathogenic bacteria; xray crystallog essential protein pathogenic

bacteria; cloning essential protein pathogenic bacteria

IT Molecular chaperones

(DnaK, protein-protein interactions of; cloning and phys.

characterization of microbial **polypeptides** involved in

protein synthesis and modification and their use as antimicrobial targets)

IT Elongation factors (protein formation)

(EF-G; cloning and phys. characterization of microbial

polypeptides involved in protein synthesis and

- modification and their use as antimicrobial targets)
- IT Ribosomal proteins
(L6, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Termination factors (protein formation)
(RF-2 (release factor 2); cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Ribosomal proteins
(S2, protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Antibacterial agents
Cryoprotectants
Crystallization
DNA sequences
Drug design
Drug screening
Drug targets
Enterococcus faecalis
Epitopes
Escherichia coli
Haemophilus influenzae
Mass spectrometry
Molecular cloning
NMR spectroscopy
Pathogenic bacteria
Protein sequences
Pseudomonas aeruginosa
Staphylococcus aureus
Streptococcus pneumoniae
(cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Hydrocarbon oils
Polyoxyalkylenes, uses
(cryoprotectant; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Solvents
(**deuterium** lock, for NMR spectroscopy; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Fusion proteins (chimeric proteins)

(for improved soly. or stability; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)

- IT Elements
(heavy, for **mass spectrometry**; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Proteins
(in protein synthesis and modification; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Flagellins
(protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Molecular association
(protein-protein; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT Crystallography
(x-ray; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 12184-88-2, Hydride 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses
(NMR **isotope**; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT 612099-21-5P 612099-23-7P 612099-25-9P 612099-27-1P
612099-29-3P 612099-31-7P 612099-33-9P 612099-35-1P
612099-37-3P 612099-39-5P 612099-41-9P 612099-43-1P
612099-46-4P 612099-48-6P 612099-50-0P 612099-52-2P
612099-54-4P 612099-56-6P 612099-58-8P 612099-60-2P
612099-62-4P 612099-64-6P 612099-67-9P 612099-70-4P 612099-7
3-7P 612099-75-9P 612549-61-8P 612549-63-0P
(amino acid sequence; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT 9037-62-1P, Glycyl-tRNA synthetase 9055-66-7P, Phenylalanyl-tRNA synthetase 9068-78-4P, Histidyl-tRNA synthetase 37257-00-4P, TRNA (guanine-7-)methyltransferase 39391-17-8P, TRNA

5-aminomethyl-2-thiouridylate 5'-methyltransferase 61229-81-0P,
Methionine aminopeptidase 129430-53-1P, O-Sialoglycoprotein
endopeptidase

(cloning and phys. characterization of microbial
polypeptides involved in protein synthesis and
modification and their use as antimicrobial targets)

IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0,
Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene
glycol, uses 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3,

Polyethylene glycol

(cryoprotectant; cloning and phys. characterization of microbial
polypeptides involved in protein synthesis and
modification and their use as antimicrobial targets)

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 917-96-4,
Methyl-d3 isocyanide 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 1735-17-7, Cyclohexane-d12
2037-26-5 2206-27-1, Dimethyl sulfoxide-d6
2679-89-2, Diethyl-d10 ether 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6,
Dimethyl-d6 ether

(deuterium lock solvent for NMR spectroscopy; cloning
and phys. characterization of microbial **polypeptides**
involved in protein synthesis and modification and their use as
antimicrobial targets)

IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9,
Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses
7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7,
Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium,
uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses
7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses
7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9,
Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium,
uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses
7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4,
Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses
7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1,
Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses
7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5,
Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses
7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2,
Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses

(heavy atom for **mass spectrometry**; cloning
and phys. characterization of microbial **polypeptides**
involved in protein synthesis and modification and their use as
antimicrobial targets)

- IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs.
 (mass spectrometry of; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT 612099-20-4, DNA (Staphylococcus aureus gene ycfB) 612099-22-6, DNA (Staphylococcus aureus gene ygiD) 612099-24-8, DNA (Staphylococcus aureus gene ygiD) 612099-26-0, DNA (Streptococcus pneumoniae gene glyQ) 612099-28-2, DNA (Streptococcus pneumoniae gene glyQ) 612099-30-6, DNA (Streptococcus pneumoniae gene yrdC) 612099-32-8, DNA (Streptococcus pneumoniae gene yrdC) 612099-34-0, DNA (Enterococcus faecalis gene fusa) 612099-36-2, DNA (Enterococcus faecalis gene fusa) 612099-38-4, DNA (Pseudomonas aeruginosa gene ygjD) 612099-40-8, DNA (Pseudomonas aeruginosa gene ygjD) 612099-42-0, DNA (Pseudomonas aeruginosa gene map) 612099-44-2, DNA (Pseudomonas aeruginosa gene map) 612099-45-3, DNA (Streptococcus pneumoniae gene fusa) 612099-47-5, DNA (Streptococcus pneumoniae gene fusa) 612099-49-7, DNA (Enterococcus faecalis gene pheS) 612099-51-1, DNA (Enterococcus faecalis gene pheS) 612099-53-3, DNA (Escherichia coli gene prfB) 612099-55-5, DNA (Escherichia coli gene prfB) 612099-57-7, DNA (Escherichia coli gene trmD) 612099-59-9, DNA (Escherichia coli gene trmD) 612099-61-3, DNA (Enterococcus faecalis gene map) 612099-63-5, DNA (Enterococcus faecalis gene map) 612099-65-7, DNA (Haemophilus influenzae gene SYH) 612099-66-8, DNA (Haemophilus influenzae gene map) 612099-68-0, DNA (Haemophilus influenzae gene map) 612099-69-1, DNA (Staphylococcus aureus gene map) 612099-71-5, DNA (Staphylococcus aureus gene map) 612099-72-6, DNA (Streptococcus pneumoniae gene map) 612099-74-8, DNA (Streptococcus pneumoniae gene map) 612549-62-9, DNA (Haemophilus influenzae gene SYH)
 (nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT 3211-76-5, Selenomethionine
 (protein label for mass spectrometry; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT 9027-73-0, 5'-Nucleotidase 9075-65-4, Glycerol-3-phosphate dehydrogenase 394250-11-4, Oligopeptidase A
 (protein-protein interactions of; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)
- IT 612100-55-7 612100-56-8 612100-57-9 612100-58-0 612100-60-4
 612100-61-5 612100-62-6 612100-63-7 612100-64-8 612100-65-9

612100-66-0	612100-67-1	612100-68-2	612100-69-3	612100-70-6
612100-71-7	612100-72-8	612100-73-9	612100-75-1	612100-76-2
612100-77-3	612100-78-4	612100-79-5	612100-80-8	612100-81-9
612100-82-0	612100-83-1	612100-84-2	612100-85-3	612100-86-4
612100-87-5	612100-88-6			

(unclaimed nucleotide sequence; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)

IT 612100-74-0

(unclaimed protein sequence; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)

IT	612077-64-2	612077-66-4	612077-68-6	612077-70-0	612077-72-2
	612077-74-4	612077-76-6	612077-78-8	612077-80-2	612077-82-4
	612077-84-6	612077-86-8	612077-88-0	612077-90-4	612077-92-6
	612077-95-9	612077-97-1	612077-99-3	612078-01-0	612078-02-1
	612078-03-2	612078-05-4	612078-07-6	612078-09-8	612078-11-2
	612078-15-6	612078-17-8	612078-19-0	612078-21-4	612078-23-6
	612078-25-8	612078-27-0	612078-29-2	612078-31-6	612078-33-8
	612078-35-0	612078-37-2	612078-39-4	612078-41-8	612078-43-0
	612078-45-2	612078-46-3	612078-48-5	612078-50-9	612078-52-1
	612100-59-1				

(unclaimed sequence; cloning and phys. characterization of microbial **polypeptides** involved in protein synthesis and modification and their use as antimicrobial targets)

L101 ANSWER 10 OF 28 HCA COPYRIGHT 2004 ACS on STN

139:210352 Isolation and **isotope** labeling of **cysteine**

- and methionine-containing tryptic **peptides**: Application to the study of cell surface proteolysis. Shen, Min; Guo, Lin; Wallace, Alison; Fitzner, Jeff; Eisenman, June; Jacobson, Erik; Johnson, Richard S. (Amgen Corporation, Seattle, WA, 98101-2936, USA). Molecular and Cellular Proteomics, 2(5), 315-324 (English) 2003. CODEN: MCPOBS. ISSN: 1535-9476. Publisher: American Society for Biochemistry and Molecular Biology.

AB Inexpensive methods were developed for isolating and **isotopically** labeling tryptic **peptides** that contain either **cysteine** or methionine. After covalently capturing **cysteine**-contg. **peptides** with pyridyl **disulfide** reactive groups on agarose beads, extensive wash steps were applied, and the attached **peptides** were released using a reducing agent. This approach results in less nonspecifically bound **peptides** and eliminates the possibility of generating avidin **peptide** background ions that can arise when using methods based on biotin and avidin (e.g. **isotope**-coded affinity tag). The thiols were alkylated using either N-ethyl- or N-D5-ethyl-iodoacetamide, both of which can

be synthesized in a single step using inexpensive reagents. This **isotopic** labeling does not greatly increase the **peptide** mass, nor does it affect the **peptide** ion charge state in electrospray ionization. In addn., methionine-contg. **peptides** were captured using com. available methionine-reactive beads, and relative quantitation of **peptides** was achieved by **isotopic** labeling of amino groups using activated esters of either nicotinic acid or D4-nicotinic acid. These methods were used to study the metalloprotease-mediated shedding of cell surface proteins from a mouse monocyte cell line that had been treated with a phorbol ester and lipopolysaccharide. In addn. to the **identification** of **proteins** previously **detd.** to be inducibly shed, three new shed **proteins** were **identified**: CD18, ICOS ligand, and tumor endothelial marker 7-related protein.

CC 9-16 (Biochemical Methods)

ST isolation **isotope** labeling cell surface **protein**
detn

IT Cell membrane

Protein degradation

(isolation and **isotope** labeling of **cysteine**-
and methionine-contg. tryptic **peptides** for **detn** of cell
surface proteins)

IT **Peptides**, analysis

Proteins

(isolation and **isotope** labeling of **cysteine**-
and methionine-contg. tryptic **peptides** for **detn** of cell
surface proteins)

IT Integrins

(.beta.2; isolation and **isotope** labeling of
cysteine- and methionine-contg. tryptic **peptides**
for **detn** of cell surface proteins)

L101 ANSWER 11; OF 28 HCA COPYRIGHT 2004 ACS on STN

139:18838 Bacterial **polypeptides** involved in general

metabolism and their characterization as antimicrobial targets.

Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad
Zahoor; Awrey, Donald; Beattie, Bryan; Canadien, Veronica; Domagala,
Megan; Houston, Simon; Li, Qin; Mansoury, Kamran; Necakov, Sasha;
Nethery, Kathleen; Ouyang, Hui; Pinder, Benjamin; Sheldrick, Bay;
Vallee, Francois; Wrezel, Olga (Affinium Pharmaceuticals, Inc.,
Can.; et al.). PCT Int. Appl. WO 2003045986 A2 20030605, 272 pp.

DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR,
BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI,
GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,
LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ,
OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR,
TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ,

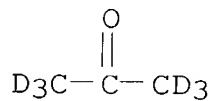
MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-CA1785 20021126. PRIORITY: US 2001-PV333340 20011126; US 2001-PV333414 20011126; US 2001-PV333423 20011126; US 2001-PV333419 20011126; US 2001-PV333342 20011126; US 2001-PV341951 20011219; US 2001-PV342558 20011220; US 2001-PV342557 20011220; US 2001-PV343613 20011228; US 2001-PV344272 20011228.

AB The present invention relates to ten **polypeptide** targets for pathogenic bacteria. The invention also provides biochem. and biophys. characteristics of those **polypeptides**. Reliable, high throughput methods are developed to identify, express, and purify a no. of antimicrobial targets from *Escherichia coli*, *Staphylococcus aureus*, *Helicobacter pylori*, *Staphylococcus pneumoniae*, and *Pseudomonas aeruginosa*. The invention provides the nucleic acid and amino acid sequences of glucose-inhibited division protein from *E. coli*, fructose biphosphate aldolase from *S. aureus*, replicative DNA helicase primosome component from *H. pylori*, protein factor essential for expression of methicillin resistance from *S. aureus*, glucosamine-fructose-6-phosphate aminotransferase from *S. aureus*, N utilization substance protein B from *S. pneumoniae*, N utilization substance protein A from *P. aeruginosa*, putative GTP-binding protein from *G. aeruginosa*, 2-dehydro-3-deoxyphosphooctonate aldolase from *P. aeruginosa*, and putative GTP-binding protein in thiophene and furan oxidn. from *S. aureus*. The invention also provides purified, sol. forms of **polypeptides** suitable for structural and functional characterization using a variety of techniques, including, for example, affinity chromatog., mass spectrometry, NMR, and x-ray crystallog. The invention further provides modified versions of the **polypeptides** to facilitate characterization, including **polypeptides** labeled with isotopic or heavy atoms and fusion proteins. One or more crystd. forms of the **polypeptides** may also be provided.

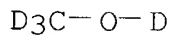
IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Deutero-chloroform 1076-43-3
, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5
1693-74-9, Tetrahydrofuran-d8 2037-26-5
2206-26-0, Acetonitrile-d3 2206-27-1
2679-89-2, Diethyl ether-d10 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6

(NMR deuterium lock solvent; bacterial
polypeptides involved in general metab. and their
characterization as antimicrobial targets)

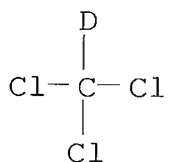
RN 666-52-4 HCA
CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



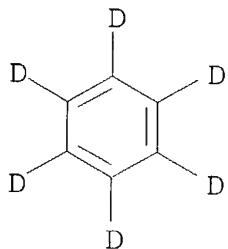
RN 811-98-3 HCA
CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



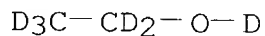
RN 865-49-6 HCA
CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



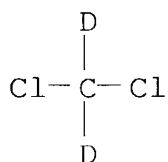
RN 1076-43-3 HCA
CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



RN 1516-08-1 HCA
CN Ethanol-d6 (9CI) (CA INDEX NAME)

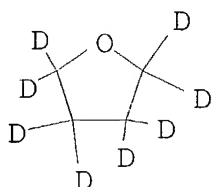


RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



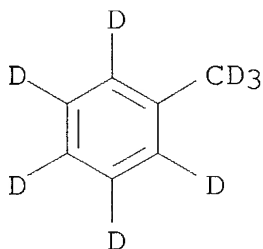
RN 1693-74-9 HCA

CN Furan-d₄, tetrahydro-d₄- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



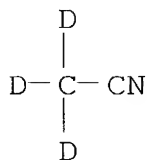
RN 2037-26-5 HCA

CN Benzene-d₅, methyl-d₃- (9CI) (CA INDEX NAME)



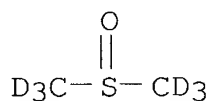
RN 2206-26-0 HCA

CN Acetonitrile-d₃ (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

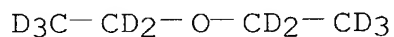


RN 2206-27-1 HCA

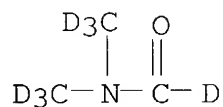
CN Methane-d₃, sulfinylbis- (9CI) (CA INDEX NAME)



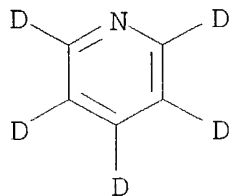
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



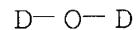
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



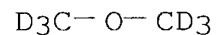
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IT 7782-39-0, Hydrogen-2, analysis
 (NMR **isotope** label; bacterial **polypeptides**
 involved in general metab. and their characterization as
 antimicrobial targets)
 RN 7782-39-0 HCA

CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IC ICM C07K014-195
CC 6-3 (General Biochemistry)
Section cross-reference(s): 1, 3, 7, 9, 10
ST protein gene metab bacteria antimicrobial target; **mass spectrometry protein** antimicrobial target; NMR **spectrometry protein** antimicrobial target; x ray crystallog protein antimicrobial target
IT Enzymes, biological studies
(DNA helicase; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
IT Proteins
(GTP-binding; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
IT Proteins
(Gene femA (Methicillin resistance protein); bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
IT Proteins
(Gene trmE (GTP-binding protein in thiophene and furan oxidn.); bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
IT Proteins
(GidB (glucose-inhibited division protein B); bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
IT Gene, microbial
(KD08PS; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
IT Affinity chromatography
Antimicrobial agents
Bacteria (Eubacteria)
Cryoprotectants
Crystallization
Drug design
Drug targets
Epitopes
Escherichia coli
Helicobacter pylori
Mass spectrometry
Molecular cloning
NMR spectroscopy

- Pseudomonas aeruginosa
Staphylococcus aureus
Streptococcus pneumoniae
 (bacterial **polypeptides** involved in general metab. and
 their characterization as antimicrobial targets)
- IT Proteins
 (bacterial **polypeptides** involved in general metab. and
 their characterization as antimicrobial targets)
- IT Fusion proteins (chimeric proteins)
 (bacterial **polypeptides** involved in general metab. and
 their characterization as antimicrobial targets)
- IT Hydrocarbon oils
 Polyoxyalkylenes, analysis
 (cryoprotectant; bacterial **polypeptides** involved in
 general metab. and their characterization as antimicrobial
 targets)
- IT Gene, microbial
 (dnaB gene; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT DNA formation factors
 (dnaB; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Gene, microbial
 (fbaA; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Gene, microbial
 (femA; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Gene, microbial
 (gidB; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Gene, microbial
 (glmS; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Transcription factors
 (nusA (N utilization substance A); bacterial **polypeptides**
 involved in general metab. and their characterization as
 antimicrobial targets)
- IT Gene, microbial
 (nusA; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Transcription factors
 (nusB; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Gene, microbial
 (nusB; bacterial **polypeptides** involved in general
 metab. and their characterization as antimicrobial targets)
- IT Conformation

- (three-dimensional structure; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
- IT Gene, microbial
(trmE; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
- IT Crystallography
(x-ray; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
- IT Gene, microbial
(ychF; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)
- IT 110-82-7, Cyclohexane, analysis 666-52-4,
2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4
865-49-6, Deutero-chloroform 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 2037-26-5 2206-26-0,
Acetonitrile-d3 2206-27-1 2679-89-2, Diethyl
ether-d10 4472-41-7, N,N-Dimethylformamide-d7
7291-22-7, Pyridine-d5 7789-20-0,
Deuterium oxide 17222-37-6
(NMR **deuterium** lock solvent; bacterial
polypeptides involved in general metab. and their
characterization as antimicrobial targets)
- IT 7440-23-5, Sodium-23, analysis 7723-14-0, Phosphorus-31, analysis
7727-37-9, Nitrogen-14, analysis 7782-39-0, Hydrogen-2,
analysis 7782-41-4, Fluorine-19, analysis 10028-17-8,
Hydrogen-3, analysis 12184-88-2, Hydride 14390-96-6,
Nitrogen-15, analysis 14762-74-4, Carbon-13, analysis
(NMR **isotope** label; bacterial **polypeptides**
involved in general metab. and their characterization as
antimicrobial targets)
- IT 538409-36-8P, Protein (Escherichia coli gene gidB) 538409-37-9P,
Protein (Escherichia coli gene gidB) 538409-39-1P 538409-41-5P
538409-43-7P 538409-45-9P 538409-47-1P 538409-48-2P
538409-50-6P 538409-52-8P 538409-54-0P 538409-56-2P
538409-58-4P 538409-61-9P 538409-63-1P 538409-65-3P
538409-67-5P 538409-69-7P 538409-70-0P
(amino acid sequence; bacterial **polypeptides** involved
in general metab. and their characterization as antimicrobial
targets)
- IT 9024-52-6P, Fructose bisphosphate aldolase 9026-96-4P,
2-Keto-3-deoxy-8-phosphooctonic synthetase 9030-45-9P,
Glucosamine-fructose-6-phosphate aminotransferase
(bacterial **polypeptides** involved in general metab. and
their characterization as antimicrobial targets)
- IT 56-81-5, Glycerol, analysis 64-18-6, Formic acid, analysis
67-63-0, Isopropanol, analysis 77-92-9, Citric acid, analysis

107-21-1, Ethylene glycol, analysis 107-41-5, 2-Methyl
2,4-pentanediol 25322-68-3, **Polyethylene glycol**
(cryoprotectant; bacterial **polypeptides** involved in
general metab. and their characterization as antimicrobial
targets)

IT 3211-76-5, Selenomethionine 7429-91-6, Dysprosium, analysis
7439-88-5, Iridium, analysis 7439-90-9, Krypton, analysis
7439-91-0, Lanthanum, analysis 7439-92-1, Lead, analysis
7439-94-3, Lutetium, analysis 7439-97-6, Mercury, analysis
7439-98-7, Molybdenum, analysis 7440-00-8, Neodymium, analysis
7440-04-2, Osmium, analysis 7440-05-3, Palladium, analysis
7440-06-4, Platinum, analysis 7440-10-0, Praseodymium, analysis
7440-15-5, Rhenium, analysis 7440-16-6, Rhodium, analysis
7440-18-8, Ruthenium, analysis 7440-19-9, Samarium, analysis
7440-22-4, Silver, analysis 7440-24-6, Strontium, analysis
7440-25-7, Tantalum, analysis 7440-27-9, Terbium, analysis
7440-28-0, Thallium, analysis 7440-29-1, Thorium, analysis
7440-30-4, Thulium, analysis 7440-31-5, Tin, analysis 7440-33-7,
Tungsten, analysis 7440-39-3, Barium, analysis 7440-43-9,
Cadmium, analysis 7440-45-1, Cerium, analysis 7440-48-4, Cobalt,
analysis 7440-52-0, Erbium, analysis 7440-53-1, Europium,
analysis 7440-54-2, Gadolinium, analysis 7440-57-5, Gold,
analysis 7440-60-0, Holmium, analysis 7440-61-1, Uranium,
analysis 7440-63-3, Xenon, analysis 7440-64-4, Ytterbium,
analysis 7553-56-2, Iodine, analysis 7726-95-6, Bromine,
analysis 7782-49-2, Selenium, analysis

(label suitable for **mass spectrometry**;

bacterial **polypeptides** involved in general metab. and
their characterization as antimicrobial targets)

IT 59-67-6D, Nicotinic acid, protein derivs. 621-82-9D, Cinnamic
acid, protein derivs.

(matrix suitable for **mass spectrometry**;

bacterial **polypeptides** involved in general metab. and
their characterization as antimicrobial targets)

IT 538409-35-7, DNA (Escherichia coli gene gidB) 538409-38-0, DNA
(Staphylococcus aureus gene fbaA) 538409-40-4, DNA (Staphylococcus
aureus gene fbaA) 538409-42-6, DNA (Helicobacter pylori gene dnaB)
538409-44-8, DNA (Helicobacter pylori gene dnaB) 538409-46-0, DNA
(Staphylococcus aureus gene femA) 538409-49-3, DNA (Staphylococcus
aureus gene glmS) 538409-51-7, DNA (Staphylococcus aureus gene
glmS) 538409-53-9 538409-55-1 538409-57-3, DNA (Pseudomonas
aeruginosa gene nusA) 538409-59-5, DNA (Pseudomonas aeruginosa
gene nusA) 538409-60-8, DNA (Pseudomonas aeruginosa gene ychF)
538409-62-0, DNA (Pseudomonas aeruginosa gene ychF) 538409-64-2,
DNA (Pseudomonas aeruginosa gene DK08PS) 538409-66-4, DNA
(Pseudomonas aeruginosa gene DK08PS) 538409-68-6, DNA
(Staphylococcus aureus gene trmE)

(nucleotide sequence; bacterial **polypeptides** involved

in general metab. and their characterization as antimicrobial targets)

IT	538419-19-1	538419-20-4	538419-33-9	538419-34-0	538419-46-4
	538419-47-5	538419-54-4	538419-55-5	538419-70-4	538419-71-5
	538419-81-7	538419-82-8	538419-91-9	538419-93-1	538420-02-9
	538420-03-0	538420-11-0	538420-13-2	538420-21-2	538420-22-3

(unclaimed nucleotide sequence; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)

IT	356063-59-7	503534-87-0	503534-88-1	538366-78-8	538366-80-2
	538366-82-4	538366-84-6	538366-86-8	538366-88-0	538366-90-4
	538366-92-6	538366-93-7	538366-94-8	538366-95-9	538366-96-0
	538366-97-1	538366-98-2	538367-00-9	538367-01-0	538367-02-1
	538367-03-2	538367-04-3	538367-05-4	538367-06-5	538367-07-6
	538367-08-7	538367-09-8	538367-10-1	538367-11-2	538367-12-3
	538367-13-4	538419-64-6	538419-74-8		

(unclaimed sequence; bacterial **polypeptides** involved in general metab. and their characterization as antimicrobial targets)

L101 ANSWER 12 OF 28 HCA COPYRIGHT 2004 ACS on STN

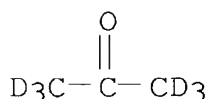
139:18837 Bacterial **polypeptides** involved in carbohydrate and coenzyme metabolism and their characterization as antimicrobial targets. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Ng, Ivy; Alam, Muhammad Zahoor; Awrey, Donald; Beattie, Bryan; Domagala, Megan; Mansoury, Kamran; Pinder, Benjamin (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003045985 A2 20030605, 191 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-CA1784 20021126. PRIORITY: US 2001-PV333349 20011126; US 2001-PV333420 20011126; US 2001-PV341950 20011219; US 2001-PV343643 20011228.

AB The present invention relates to ten **polypeptide** targets for pathogenic bacteria. The invention also provides biochem. and biophys. characteristics of those **polypeptides**. Reliable, high throughput methods are developed to identified, express, and purify a no. of antimicrobial targets from Escherichia coli, Staphylococcus aureus, and Pseudomonas aeruginosa. The invention provides the nucleic acid and amino acid sequences of phosphoglycerate kinase from S. aureus, flavoprotein affectin synthesis of DNA and pantothenate from E. coli, riboflavin kinase/FAD synthase from S. aureus, and phosphopantetheine

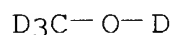
adenylyltransferase from *P. aeruginosa*. The invention also provides purified, sol. forms of **polypeptides** suitable for structural and functional characterization using a variety of techniques, including, for example, affinity chromatog., **mass spectrometry**, NMR, and x-ray crystallog. The invention further provides modified versions of the **polypeptides** to facilitate characterization, including **polypeptides** labeled with **isotopic** or heavy atoms and fusion proteins. One or more crystd. forms of the **polypeptides** may also be provided.

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Deutero-chloroform 1076-43-3
, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5
1693-74-9, Tetrahydrofuran-d8 2037-26-5
2206-26-0, Acetonitrile-d3 2206-27-1
2679-89-2, Diethyl ether-d10 4472-41-7,
N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5
7789-20-0, Deuterium oxide 17222-37-6
(NMR deuterium lock solvent; bacterial
polypeptides involved in carbohydrate and coenzyme metab.
and their characterization as antimicrobial targets)

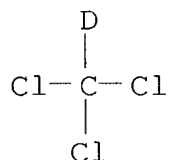
RN 666-52-4 HCA
CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



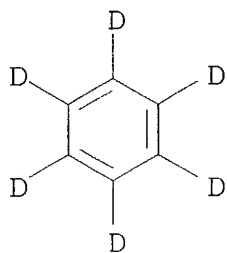
RN 811-98-3 HCA
CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



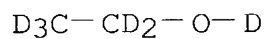
RN 865-49-6 HCA
CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



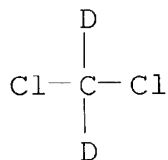
RN 1076-43-3 HCA
CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



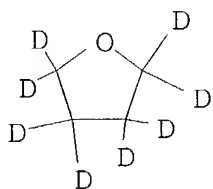
RN 1516-08-1 HCA
CN Ethanol-d6 (9CI) (CA INDEX NAME)



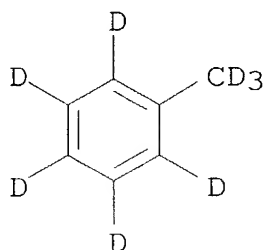
RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



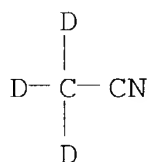
RN 1693-74-9 HCA
CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



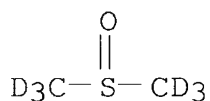
RN 2037-26-5 HCA
CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



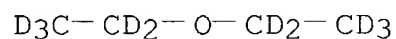
RN 2206-26-0 HCA
 CN Acetonitrile-d3 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



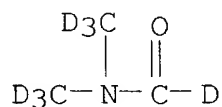
RN 2206-27-1 HCA
 CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



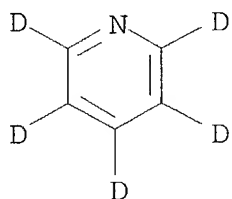
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)

D-O-D

RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)

D₃C-O-CD₃

IT 7782-39-0, Hydrogen-2, analysis
 (NMR **isotope** label; bacterial **polypeptides**
 involved in carbohydrate and coenzyme metab. and their
 characterization as antimicrobial targets)
 RN 7782-39-0 HCA
 CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IC ICM C07K014-195
 CC 6-3 (General Biochemistry)
 Section cross-reference(s): 1, 3, 7, 9, 10
 ST protein gene metab bacteria antimicrobial target; **mass**
spectrometry protein antimicrobial target; NMR
spectrometry protein antimicrobial target; x ray
 crystallog protein antimicrobial target
 IT Affinity chromatography
 Antimicrobial agents
 Bacteria (Eubacteria)
 Cryoprotectants
 Crystallization
 Drug design
 Drug targets
 Epitopes
 Escherichia coli
 Helicobacter pylori

Mass spectrometry

Molecular cloning

NMR spectroscopy

Pseudomonas aeruginosa

Staphylococcus aureus

Streptococcus pneumoniae

(bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Proteins

(bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Fusion proteins (chimeric proteins)

(bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Gene, microbial

(coaD; bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Hydrocarbon oils

Polyoxyalkylenes, analysis

(cryoprotectant; bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Gene, microbial

(dfp; bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Flavoproteins

(gene dfp; bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Gene, microbial

(pgk; bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Gene, microbial

(ribC; bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Conformation

(three-dimensional structure; bacterial **polypeptides** involved in carbohydrate and coenzyme metab. and their characterization as antimicrobial targets)

IT Crystallography

(x-ray; bacterial **polypeptides** involved in carbohydrate

and coenzyme metab. and their characterization as antimicrobial targets)

- IT 110-82-7, Cyclohexane, analysis 666-52-4,
2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4
865-49-6, Deutero-chloroform 1076-43-3, Benzene-d6
1516-08-1, Ethanol-d6 1665-00-5 1693-74-9
, Tetrahydrofuran-d8 2037-26-5 2206-26-0,
Acetonitrile-d3 2206-27-1 2679-89-2, Diethyl
ether-d10 4472-41-7, N,N-Dimethylformamide-d7
7291-22-7, Pyridine-d5 7789-20-0,
Deuterium oxide 17222-37-6
(NMR **deuterium** lock solvent; bacterial
polypeptides involved in carbohydrate and coenzyme metab.
and their characterization as antimicrobial targets)
- IT 7440-23-5, Sodium-23, analysis 7723-14-0, Phosphorus-31, analysis
7727-37-9, Nitrogen-14, analysis 7782-39-0, Hydrogen-2,
analysis 7782-41-4, Fluorine-19, analysis 10028-17-8,
Hydrogen-3, analysis 12184-88-2, Hydride 14390-96-6,
Nitrogen-15, analysis 14762-74-4, Carbon-13, analysis
(NMR **isotope** label; bacterial **polypeptides**
involved in carbohydrate and coenzyme metab. and their
characterization as antimicrobial targets)
- IT 538410-08-1P 538410-10-5P 538410-12-7P, Flavoprotein
(Escherichia coli gene dfp) 538410-14-9P, Flavoprotein
(Escherichia coli gene dfp) 538410-16-1P 538410-17-2P
538410-19-4P
(amino acid sequence; bacterial **polypeptides** involved
in carbohydrate and coenzyme metab. and their characterization as
antimicrobial targets)
- IT 9001-83-6P, Phosphoglycerate kinase 9026-37-3P, FAD synthetase
9026-99-7P, Phosphopantetheine adenylyltransferase 9032-82-0P,
Riboflavin kinase
(bacterial **polypeptides** involved in carbohydrate and
coenzyme metab. and their characterization as antimicrobial
targets)
- IT 56-81-5, Glycerol, analysis 64-18-6, Formic acid, analysis
67-63-0, Isopropanol, analysis 77-92-9, Citric acid, analysis
107-21-1, Ethylene glycol, analysis 107-41-5, 2-Methyl
2,4-pentanediol 25322-68-3, **Polyethylene glycol**
(cryoprotectant; bacterial **polypeptides** involved in
carbohydrate and coenzyme metab. and their characterization as
antimicrobial targets)
- IT 3211-76-5, Selenomethionine 7429-91-6, Dysprosium, analysis
7439-88-5, Iridium, analysis 7439-90-9, Krypton, analysis
7439-91-0, Lanthanum, analysis 7439-92-1, Lead, analysis
7439-94-3, Lutetium, analysis 7439-97-6, Mercury, analysis
7439-98-7, Molybdenum, analysis 7440-00-8, Neodymium, analysis
7440-04-2, Osmium, analysis 7440-05-3, Palladium, analysis

7440-06-4, Platinum, analysis 7440-10-0, Praseodymium, analysis
 7440-15-5, Rhenium, analysis 7440-16-6, Rhodium, analysis
 7440-18-8, Ruthenium, analysis 7440-19-9, Samarium, analysis
 7440-22-4, Silver, analysis 7440-24-6, Strontium, analysis
 7440-25-7, Tantalum, analysis 7440-27-9, Terbium, analysis
 7440-28-0, Thallium, analysis 7440-29-1, Thorium, analysis
 7440-30-4, Thulium, analysis 7440-31-5, Tin, analysis 7440-33-7,
 Tungsten, analysis 7440-39-3, Barium, analysis 7440-43-9,
 Cadmium, analysis 7440-45-1, Cerium, analysis 7440-48-4, Cobalt,
 analysis 7440-52-0, Erbium, analysis 7440-53-1, Europium,
 analysis 7440-54-2, Gadolinium, analysis 7440-57-5, Gold,
 analysis 7440-60-0, Holmium, analysis 7440-61-1, Uranium,
 analysis 7440-63-3, Xenon, analysis 7440-64-4, Ytterbium,
 analysis 7553-56-2, Iodine, analysis 7726-95-6, Bromine,
 analysis 7782-49-2, Selenium, analysis

(label suitable for **mass spectrometry**;

bacterial **polypeptides** involved in carbohydrate and
 coenzyme metab. and their characterization as antimicrobial
 targets)

IT 59-67-6D, Nicotinic acid, protein derivs. 621-82-9D, Cinnamic
 acid, protein derivs.

(matrix suitable for **mass spectrometry**;

bacterial **polypeptides** involved in carbohydrate and
 coenzyme metab. and their characterization as antimicrobial
 targets)

IT 538410-07-0, DNA (Staphylococcus aureus gene pgk) 538410-09-2, DNA
 (Staphylococcus aureus gene pgk) 538410-11-6, DNA (Escherichia
 coli gene dfp) 538410-13-8, DNA (Escherichia coli gene dfp)
 538410-15-0, DNA (Staphylococcus aureus gene ribC) 538410-18-3,
 DNA (Pseudomonas aeruginosa gene coaD) 538410-20-7, DNA
 (Pseudomonas aeruginosa gene coaD)

(nucleotide sequence; bacterial **polypeptides** involved
 in carbohydrate and coenzyme metab. and their characterization as
 antimicrobial targets)

IT 538421-48-6 538421-49-7 538421-58-8 538421-59-9 538421-69-1
 538421-70-4 538421-76-0 538421-77-1

(unclaimed nucleotide sequence; bacterial **polypeptides**
 involved in carbohydrate and coenzyme metab. and their
 characterization as antimicrobial targets)

IT 503534-87-0 503534-88-1 538324-36-6 538324-37-7 538324-38-8
 538324-39-9 538324-40-2 538324-41-3 538324-42-4 538324-43-5
 538324-44-6 538324-45-7 538324-46-8 538324-47-9 538324-48-0

(unclaimed sequence; bacterial **polypeptides** involved in
 carbohydrate and coenzyme metab. and their characterization as
 antimicrobial targets)

pathogenic bacteria involved in protein processing and drug screening and drug design applications. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad Zahoor; Awrey, Donald; Beattie, Bryan; Canadien, Veronica; Domagala, Megan; Kanagarajah, Dhushy; Li, Qin; Mansoury, Kamran; Necakov, Sasha; Nethery, Kathleen; Ng, Ivy; Pinder, Benjamin; Sheldrick, Bay; Vallee, Francois; Viola, Cristina; Wrezel, Olga (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003025005 A2 20030327, 273 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-CA1426 20020920. PRIORITY: US 2001-PV324135 20010921; US 2001-PV324139 20010921; US 2001-PV325333 20010927; US 2001-PV325836 20010928; US 2001-PV338235 20011025; US 2001-PV343758 20011025; US 2001-PV340531 20011026; US 2001-PV340945 20011030; US 2001-PV333281 20011106; US 2002-PV399926 20020731.

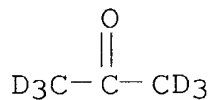
AB The present invention relates to **polypeptide** targets for pathogenic bacteria. A no. of antimicrobial target enzymes have been identified, expressed, and purified from *Staphylococcus aureus*, *Helicobacter pylori*, *Streptococcus pneumoniae*, and *Escherichia coli*. Cloning, the nucleotide sequences and the encoded amino acid sequences of genes *clpL*, *cysM*, *pepP*, *kdsA*, *secA*, *trmD*, *ilvE*, *aroB*, and *glyA* from *S. aureus*, *H. pylori*, *S. pneumoniae*, and *E. coli* are disclosed. The invention also provides biochem. and biophys. characteristics of those **polypeptides**. The **polypeptides** are characterized by using **mass spectrometry**, NMR, x-ray crystallog., and bioinformatics anal. The **polypeptides** of the invention can be used for drug screening, drug design, in diagnostic assays and in pharmacol. applications.

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 1076-43-3,
Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5
1693-74-9 2037-26-5 2206-26-0,
Acetonitrile-d3 2206-27-1 2679-89-2
4472-41-7, N,N-Dimethylformamide-d7 7291-22-7,
Pyridine-d5 7789-20-0, Water-d2
17222-37-6

(deuterium lock solvent; cloning, purifn. and characterization of enzymes from pathogenic bacteria involved in protein processing, and drug screening and drug design applications)

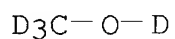
RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



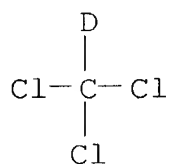
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



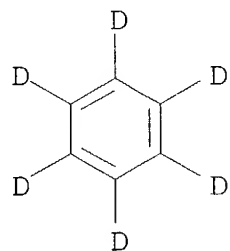
RN 865-49-6 HCA

CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



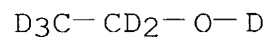
RN 1076-43-3 HCA

CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



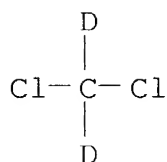
RN 1516-08-1 HCA

CN Ethanol-d6 (9CI) (CA INDEX NAME)



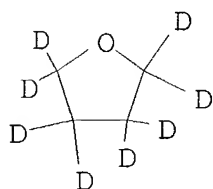
RN 1665-00-5 HCA

CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



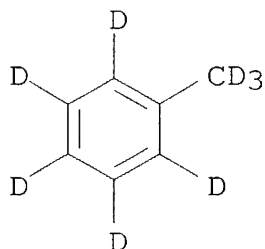
RN 1693-74-9 HCA

CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



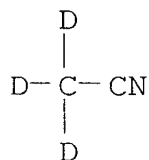
RN 2037-26-5 HCA

CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



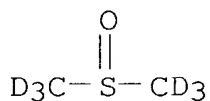
RN 2206-26-0 HCA

CN Acetonitrile-d3 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

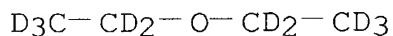


RN 2206-27-1 HCA

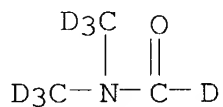
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



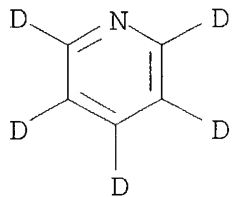
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



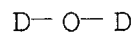
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



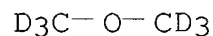
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IT 7782-39-0, Hydrogen-2, uses
 (isotope label; cloning, purifn. and characterization
 of enzymes from pathogenic bacteria involved in protein
 processing, and drug screening and drug design applications)
 RN 7782-39-0 HCA

CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IC ICM C07K014-195

CC 7-2 (Enzymes)

Section cross-reference(s): 1, 3, 10, 63

IT Antibacterial agents

Bioinformatics

Cryoprotectants

Crystal growth

Crystal morphology

DNA sequences

Drug design

Drug screening

Escherichia coli

Exchange reaction

Gel electrophoresis

Helicobacter pylori

Mass spectrometry

Molecular cloning

NMR (nuclear magnetic resonance)

NMR spectroscopy

Pathogenic bacteria

Post-translational processing

Protein sequences

Solubility

Stability

Staphylococcus aureus

Streptococcus pneumoniae

X-ray diffractometry

(cloning, purifn. and characterization of enzymes from pathogenic bacteria involved in protein processing, and drug screening and drug design applications)

IT Molecular association

(**identification** of interacting **proteins**;

cloning, purifn. and characterization of enzymes from pathogenic bacteria involved in protein processing, and drug screening and drug design applications)

IT **Polyoxyalkylenes**, uses

(low-mol.-wt., cryoprotectant; cloning, purifn. and characterization of enzymes from pathogenic bacteria involved in protein processing, and drug screening and drug design applications)

IT 110-82-7, Cyclohexane, uses 666-52-4, 2-Propanone-

1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6,

Chloroform-d 1076-43-3, Benzene-d6 1516-08-1,

Ethanol-d6 1665-00-5 1693-74-9 2037-26-5
2206-26-0, Acetonitrile-d3 2206-27-1
2679-89-2 4472-41-7, N,N-Dimethylformamide-d7
7291-22-7, Pyridine-d5 7789-20-0, Water-d2
17222-37-6

(deuterium lock solvent; cloning, purifn. and
characterization of enzymes from pathogenic bacteria involved in
protein processing, and drug screening and drug design
applications)

IT 1333-74-0, Hydrogen, uses 7440-23-5, Sodium-23, uses 7723-14-0,
Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses 7782-39-0
, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8,
Hydrogen-3, uses 14390-96-6, Nitrogen-15, uses 14762-74-4,
Carbon-13, uses

(isotope label; cloning, purifn. and characterization
of enzymes from pathogenic bacteria involved in protein
processing, and drug screening and drug design applications)

IT 25322-68-3, PEG

(low-mol.-wt., cryoprotectant; cloning, purifn. and
characterization of enzymes from pathogenic bacteria involved in
protein processing, and drug screening and drug design
applications)

IT 59-67-6D, Nicotinic acid, derivs.

(mass spectrometric matrix; cloning, purifn.
and characterization of enzymes from pathogenic bacteria involved
in protein processing, and drug screening and drug design
applications)

L101 ANSWER 14 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:283070 Purification of enzymes involved in protein synthesis from
pathogenic bacteria for characterization in development of targets
for antibiotics. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud;
Alam, Muhammad Zahoor; Awrey, Donald; Beattie, Bryan; Canadien,
Veronica; Domagala, Megan; Houston, Simon; Kanagarajah, Dhushy;
Necakov, Sasha; Nethery, Kathleen; Ng, Ivy; Mansoury, Kamran;
McDonald, Merry-Lynn; Pinder, Benjamin; Sheldrick, Bay; Viola,
Cristina (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO
2003025008 A2 20030327, 254 pp. DESIGNATED STATES: W: AE, AG, AL,
AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ,
DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD,
MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG,
SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA,
ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF,
CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC,
ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2.
APPLICATION: WO 2002-CA1429 20020920. PRIORITY: US 2001-PV324176
20010921; US 2001-PV324439 20010924; US 2001-PV324713 20010925; US

2001-PV324690 20010925; US 2001-PV326336 20011001; US 2001-PV341466 20011217; US 2001-PV341764 20011218; US 2001-PV341918 20011219.

AB Methods of purifying and characterizing enzymes that may play a role in protein synthesis in pathogenic bacteria are described. The proteins may be useful as targets for antibiotics and methods for identifying regions of the proteins that may be targeted by drugs are described. The invention also provides biochem. and biophys. characteristics of those **polypeptides**.

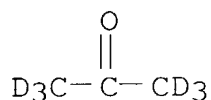
IT 666-52-4, Perdeuteroacetone 811-98-3, Methanol-d4
865-49-6, Deuteriochloroform 1076-43-3,
Perdeutero benzene 1516-08-1, Ethanol-d6 1665-00-5
1693-74-9, Perdeuterotetrahydrofuran 2037-26-5
2206-26-0, Perdeuteroacetonitrile 2206-27-1,
Dimethylsulfoxide-d6 2679-89-2, Diethyl ether-d10
4472-41-7, N,N-Dimethylformamide-d7 7291-22-7,
Pyridine-d5 7789-20-0, Heavy water 17222-37-6

(as **deuterium** lock solvent in NMR of proteins; purifn.

of enzymes involved in protein synthesis from pathogenic bacteria
for characterization in development of targets for antibiotics)

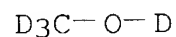
RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



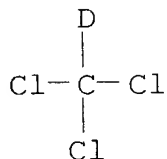
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



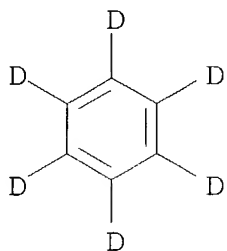
RN 865-49-6 HCA

CN Methane-d, trichloro- (9CI) (CA INDEX NAME)

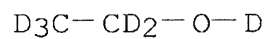


RN 1076-43-3 HCA

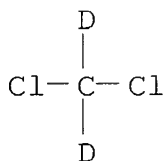
CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



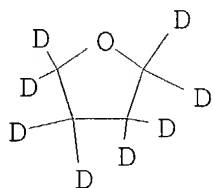
RN 1516-08-1 HCA
CN Ethanol-d6 (9CI) (CA INDEX NAME)



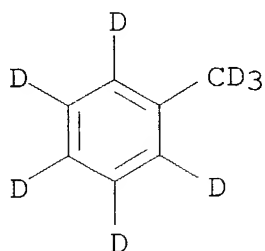
RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



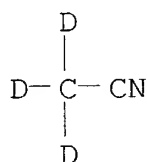
RN 1693-74-9 HCA
CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



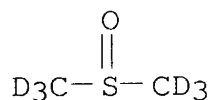
RN 2037-26-5 HCA
CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



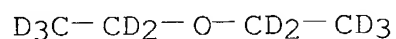
RN 2206-26-0 HCA
 CN Acetonitrile-d3 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



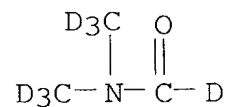
RN 2206-27-1 HCA
 CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



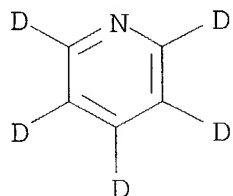
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)

D-O-D

RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)

D₃C-O-CD₃

IT 7782-39-0, **Deuterium**, biological studies
 (as **isotopic** label for NMR of proteins; purifn. of
 enzymes involved in protein synthesis from pathogenic bacteria
 for characterization in development of targets for antibiotics)
 RN 7782-39-0 HCA
 CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IC ICM C07K014-195
 CC 6-3 (General Biochemistry)
 Section cross-reference(s): 1, 3, 10
 ST enzyme purifn NMR **mass spectrometry** genomics
protein synthesis; protein processing enzyme antibiotic
 design selection
 IT Hydrocarbon oils
Polyoxyalkylenes, biological studies
 (as cryoprotectant; purifn. of enzymes involved in protein
 synthesis from pathogenic bacteria for characterization in
 development of targets for antibiotics)
 IT NMR spectroscopy
 (**deuterium**; purifn. of enzymes involved in protein
 synthesis from pathogenic bacteria for characterization in
 development of targets for antibiotics)
 IT Crystallization
Mass spectrometry

(of **proteins**; purifn. of enzymes involved in protein synthesis from pathogenic bacteria for characterization in development of targets for antibiotics)

IT 56-81-5, Glycerol, biological studies 64-18-6, Formic acid, biological studies 67-63-0, Isopropanol, biological studies 77-92-9, Citric acid, biological studies 107-21-1, Ethylene glycol, biological studies 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3, **Polyethylene glycol**

(as cryoprotectant; purifn. of enzymes involved in protein synthesis from pathogenic bacteria for characterization in development of targets for antibiotics)

IT 110-82-7, Cyclohexane, analysis 666-52-4, Perdeuteroacetone 811-98-3, Methanol-d4 865-49-6, Deuteriochloroform 1076-43-3, Perdeuterobenzene 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Perdeuterotetrahydrofuran 2037-26-5 2206-26-0, Perdeuteroacetonitrile 2206-27-1, Dimethylsulfoxide-d6 2679-89-2, Diethyl ether-d10 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, Heavy water 17222-37-6

(as **deuterium** lock solvent in NMR of proteins; purifn. of enzymes involved in protein synthesis from pathogenic bacteria for characterization in development of targets for antibiotics)

IT 1333-74-0, Hydrogen, biological studies 7440-23-5, Sodium-23, biological studies 7723-14-0, Phosphorus-31, biological studies 7727-37-9, Nitrogen 14, biological studies 7782-39-0, **Deuterium**, biological studies 7782-41-4, Fluorine-19, biological studies 10028-17-8, Tritium, biological studies 14390-96-6, Nitrogen 15, biological studies 14762-74-4, Carbon 13, biological studies

(as **isotopic** label for NMR of proteins; purifn. of enzymes involved in protein synthesis from pathogenic bacteria for characterization in development of targets for antibiotics)

L101 ANSWER 15 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:283069 Purification of proteins of microbial cell wall biosynthesis from pathogenic bacteria for characterization in development of targets for antibiotics. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad Zahoor; Awrey, Donald; Beattie, Bryan; Domagala, Megan; Houston, Simon; Kanagarajah, Dhushy; Nethery, Kathleen; Ng, Ivy; Mansoury, Kamran; McDonald, Merry-Lynn; Pinder, Benjamin; Viola, Cristina; Wrezel, Olga (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003025007 A2 20030327, 325 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT,

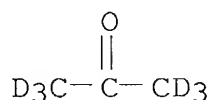
TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-CA1428 20020920. PRIORITY: US 2001-PV324152 20010921; US 2001-PV323992 20010921; US 2001-PV324692 20010925; US 2001-PV339924 20011026; US 2001-PV350973 20011029; US 2001-PV340924 20011030; US 2001-PV333666 20011127; US 2001-PV341732 20011218; US 2001-PV341776 20011218; US 2001-PV341949 20011219.

AB Methods of purifying and characterizing enzymes that may play a role in microbial cell wall biosynthesis in pathogenic bacteria are described. The proteins may be useful as targets for antibiotics and methods for identifying regions of the proteins that may be targeted by drugs are described. The invention also provides biochem. and biophys. characteristics of those **polypeptides**

IT 666-52-4, Perdeuteroacetone 811-98-3, Methanol-d4 865-49-6, Deuteriochloroform 1076-43-3, Perdeuterobenzene 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Perdeuterotetrahydrofuran 2037-26-5 2206-26-0, Perdeuteroacetonitrile 2206-27-1, Dimethylsulfoxide-d6 2679-89-2, Diethyl ether-d10 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, Heavy water 17222-37-6 (as **deuterium** lock solvent in NMR of proteins; purifn. of proteins of microbial cell wall biosynthesis from pathogenic bacteria for characterization in development of targets for antibiotics)

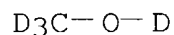
RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



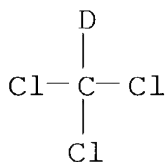
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

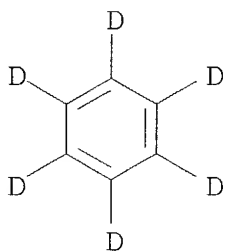


RN 865-49-6 HCA

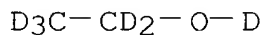
CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



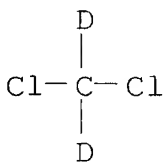
RN 1076-43-3 HCA
 CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



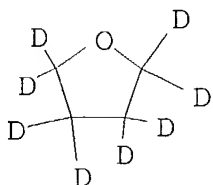
RN 1516-08-1 HCA
 CN Ethanol-d6 (9CI) (CA INDEX NAME)



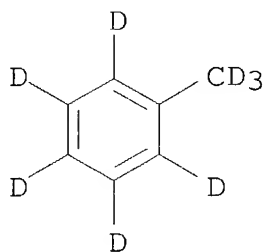
RN 1665-00-5 HCA
 CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



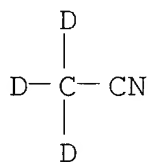
RN 1693-74-9 HCA
 CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



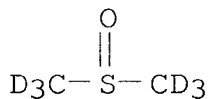
RN 2037-26-5 HCA
 CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



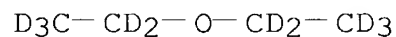
RN 2206-26-0 HCA
 CN Acetonitrile-d3 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



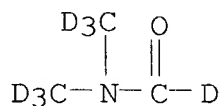
RN 2206-27-1 HCA
 CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



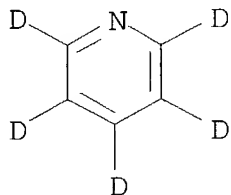
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)

D—O—D

RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)

D₃C—O—CD₃

IT 7782-39-0, **Deuterium**, biological studies
 (as **isotopic** label for NMR of proteins; purifn. of
 proteins of microbial cell wall biosynthesis from pathogenic
 bacteria for characterization in development of targets for
 antibiotics)

RN 7782-39-0 HCA
 CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D—D

IC ICM C07K014-195
 CC 6-3 (General Biochemistry)
 Section cross-reference(s): 1, 3, 10
 ST enzyme purifn NMR **mass spectrometry** genomics;
 microbial cell wall biosynthesis enzyme antibiotic design selection
 IT Hydrocarbon oils
 Polyoxyalkylenes, biological studies
 (as cryoprotectant; purifn. of proteins of microbial cell wall
 biosynthesis from pathogenic bacteria for characterization in
 development of targets for antibiotics)
 IT NMR spectroscopy
 (**deuterium**; purifn. of proteins of microbial cell wall
 biosynthesis from pathogenic bacteria for characterization in
 development of targets for antibiotics)
 IT Crystallization
 Mass spectrometry
 (of **proteins**; purifn. of proteins of microbial cell

- wall biosynthesis from pathogenic bacteria for characterization in development of targets for antibiotics)
- IT 56-81-5, Glycerol, biological studies 64-18-6, Formic acid, biological studies 67-63-0, Isopropanol, biological studies 77-92-9, Citric acid, biological studies 107-21-1, Ethylene glycol, biological studies 5683-44-3, 3-Methyl-2,4-pentanediol 25322-68-3, **Polyethylene glycol**
(as cryoprotectant; purifn. of proteins of microbial cell wall biosynthesis from pathogenic bacteria for characterization in development of targets for antibiotics)
- IT 110-82-7, Cyclohexane, analysis 666-52-4, Perdeuteroacetone 811-98-3, Methanol-d4 865-49-6, Deuteriochloroform 1076-43-3, Perdeuterobenzene 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9, Perdeuterotetrahydrofuran 2037-26-5 2206-26-0, Perdeuteroacetonitrile 2206-27-1, Dimethylsulfoxide-d6 2679-89-2, Diethyl ether-d10 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, Heavy water 17222-37-6
(as **deuterium** lock solvent in NMR of proteins; purifn. of proteins of microbial cell wall biosynthesis from pathogenic bacteria for characterization in development of targets for antibiotics)
- IT 1333-74-0, Hydrogen, biological studies 7440-23-5, Sodium-23, biological studies 7723-14-0, Phosphorus-31, biological studies 7727-37-9, Nitrogen 14, biological studies 7782-39-0, **Deuterium**, biological studies 7782-41-4, Fluorine-19, biological studies 10028-17-8, Tritium, biological studies 14390-96-6, Nitrogen 15, biological studies 14762-74-4, Carbon 13, biological studies
(as **isotopic** label for NMR of proteins; purifn. of proteins of microbial cell wall biosynthesis from pathogenic bacteria for characterization in development of targets for antibiotics)

L101 ANSWER 16 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:282444 Cloning, purification and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad Zahoor; Awrey, Donald; Beattie, Bryan; Canadien, Veronica; Domagala, Megan; Houston, Simon; Kanagarajah, Dhushy; Li, Qin; Mansoury, Kamran; McDonald, Merry-Lynn; Necakov, Sasha; Ng, Ivy; Pinder, Benjamin; Sheldrick, Bay; Vallee, Francois; Viola, Cristina; Wrezel, Olga (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003027139 A2 20030403, 312 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,

IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-CA1443 20020924. PRIORITY: US 2001-PV324449 20010924; US 2001-PV324504 20010924; US 2001-PV326269 20011001; US 2001-PV326887 20011003; US 2001-PV339560 20011024; US 2001-PV337471 20011025; US 2001-PV340002 20011026; US 2001-PV340000 20011026; US 2001-PV340027 20011026; US 2001-PV341767 20011218; US 2001-PV344307 20011221; US 2001-PV343946 20011227.

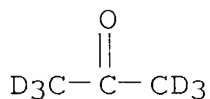
AB The present invention relates to **polypeptide** targets for pathogenic bacteria. A no. of antimicrobial target enzymes and **proteins** have been **identified**, expressed, and purified from *Staphylococcus aureus*, *Helicobacter pylori*, *Streptococcus pneumoniae*, and *Pseudomonas aeruginosa*. Cloning, the nucleotide sequences and the encoded amino acid sequences of genes *ftsZ*, *fabZ*, *acpS*, *murD*, *murC*, *fabH*, *tagD*, *obg*, and *fabG* from *S. aureus*, *H. pylori*, *S. pneumoniae*, and *P. aeruginosa* are disclosed. The invention also provides biochem. and biophys. characteristics of those **polypeptides**. The **polypeptides** are characterized by using **mass spectrometry**, NMR, x-ray crystallog., and bioinformatics anal. The **polypeptides** of the invention can be used for drug screening, drug design, in diagnostic assays and in pharmacol. applications.

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 1076-43-3,
Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5
1693-74-9 2037-26-5 2206-26-0,
Acetonitrile-d3 2206-27-1 2679-89-2
4472-41-7, N,N-Dimethylformamide-d7 7291-22-7,
Pyridine-d5 7789-20-0, Water-d2
17222-37-6

(deuterium lock solvent; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

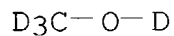
RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



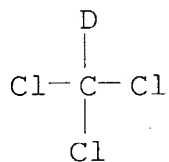
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



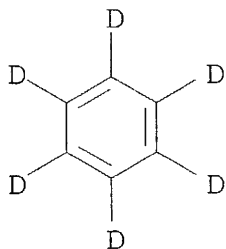
RN 865-49-6 HCA

CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



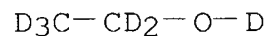
RN 1076-43-3 HCA

CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



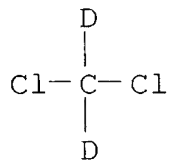
RN 1516-08-1 HCA

CN Ethanol-d6 (9CI) (CA INDEX NAME)



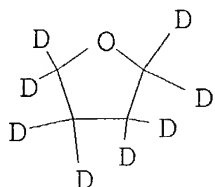
RN 1665-00-5 HCA

CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

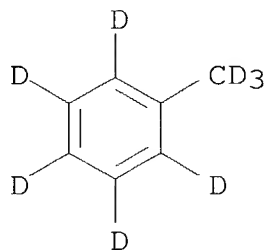


RN 1693-74-9 HCA

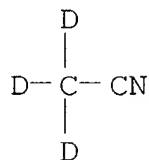
CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



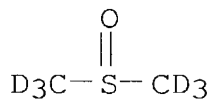
RN 2037-26-5 HCA
 CN Benzene-d₅, methyl-d₃- (9CI) (CA INDEX NAME)



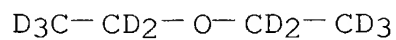
RN 2206-26-0 HCA
 CN Acetonitrile-d₃ (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



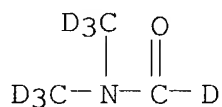
RN 2206-27-1 HCA
 CN Methane-d₃, sulfinylbis- (9CI) (CA INDEX NAME)



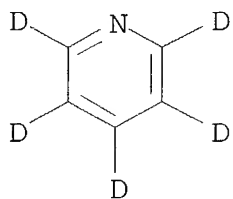
RN 2679-89-2 HCA
 CN Ethane-d₅, 2,2'-oxybis- (9CI) (CA INDEX NAME)



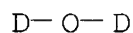
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d₃)- (7CI, 8CI, 9CI) (CA INDEX NAME)



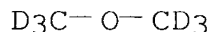
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IT 7782-39-0, Hydrogen-2, uses
 (isotope label; cloning, purifn. and characterization
 of **polypeptides** from pathogenic bacteria involved in
 membrane biosynthesis, and drug screening and drug design
 applications)

RN 7782-39-0 HCA
 CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)



IC ICM C07K014-195
 CC 3-3 (Biochemical Genetics)
 Section cross-reference(s): 1, 6, 7, 10, 63
 IT Proteins
 (16,000-mol.-wt., compn. contg. 3-Oxoacyl-[acyl carrier protein]
 synthase III and; cloning, purifn. and characterization of
polypeptides from pathogenic bacteria involved in
 membrane biosynthesis, and drug screening and drug design)

applications)

- IT Proteins
(25,000-mol.-wt., compn. contg. 3-oxoacyl-[acyl carrier protein]
reductase and; cloning, purifn. and characterization of
polypeptides from pathogenic bacteria involved in
membrane biosynthesis, and drug screening and drug design
applications)
- IT Proteins
(FTSA, compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins
(L1, compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins
(L16, compn. contg. gene obg protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins
(L2, compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins
(L22, compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins
(L3, compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins
(L4, compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins
(L5, compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT Ribosomal proteins

(L6, compn. contg. FtsZ protein and; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Ribosomal proteins
(S2, compn. contg. FtsZ protein and; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Ribosomal proteins
(S4, compn. contg. FtsZ protein and; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Ribosomal proteins
(S5, compn. contg. FtsZ protein and; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Ribosomal proteins
(S7, compn. contg. FtsZ protein and; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Gene, microbial
(acpS; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Infection
(bacterial; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Membrane, biological
(bilayer; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT Antibacterial agents
Bioinformatics
Cryoprotectants
Crystal growth
Crystal morphology
DNA sequences
Drug design
Drug screening
Exchange reaction

Gel electrophoresis

Helicobacter pylori

Mass spectrometry

Molecular cloning

NMR (nuclear magnetic resonance)

NMR spectroscopy

Pathogenic bacteria

Protein sequences

Pseudomonas aeruginosa

Solubility

Stability

Staphylococcus aureus

Streptococcus pneumoniae

X-ray diffractometry

(cloning, purifn. and characterization of **polypeptides**

from pathogenic bacteria involved in membrane biosynthesis, and

drug screening and drug design applications)

IT Fusion proteins (chimeric proteins)

(cloning, purifn. and characterization of **polypeptides**

from pathogenic bacteria involved in membrane biosynthesis, and

drug screening and drug design applications)

IT Paraffin oils

(cryoprotectant; cloning, purifn. and characterization of

polypeptides from pathogenic bacteria involved in

membrane biosynthesis, and drug screening and drug design

applications)

IT Gene, microbial

(fabG; cloning, purifn. and characterization of

polypeptides from pathogenic bacteria involved in

membrane biosynthesis, and drug screening and drug design

applications)

IT Gene, microbial

(fabH; cloning, purifn. and characterization of

polypeptides from pathogenic bacteria involved in

membrane biosynthesis, and drug screening and drug design

applications)

IT Gene, microbial

(fabZ; cloning, purifn. and characterization of

polypeptides from pathogenic bacteria involved in

membrane biosynthesis, and drug screening and drug design

applications)

IT Proteins

(ftsZ, Staphylococcus aureus; cloning, purifn. and

characterization of **polypeptides** from pathogenic

bacteria involved in membrane biosynthesis, and drug screening

and drug design applications)

IT Gene, microbial

(ftsZ; cloning, purifn. and characterization of

polypeptides from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

- IT Proteins
(gene obg, Staphylococcus aureus; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Proteins
(gene tagD, Staphylococcus aureus; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Elements
(heavy, label; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Molecular association
(**identification** of interacting **proteins**; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Toxins
(leukotoxins, LukM, compn. contg.; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT **Polyoxyalkylenes**, uses
(low-mol.-wt., cryoprotectant; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Epitopes
(mapping; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Gene, microbial
(murC; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Gene, microbial
(murD; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

- IT Gene, microbial
(obg; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Organic compounds, biological studies
(**polypeptides** complexed with; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Conformation
(protein; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Gene, microbial
(tagD; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT Genome
(virtual genome anal.; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT 9030-86-8P, (3R)-Hydroxymyristoyl-[acyl-carrier protein] dehydratase
((3R)-Hydroxymyristoyl-[acyl-carrier protein] dehydratase, of *Staphylococcus aureus*; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT 9023-52-3P, Gene murC enzyme 9023-59-0P, UDP-N-acetylmuramoylalanine-D-glutamate ligase
(*H. pylori*; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT 37250-34-3P, 3-Ketoacyl acyl carrier protein reductase
(*Helicobacter pylori* and *Pseudomonas aeruginosa*; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT 9077-10-5P, 3-Oxoacyl-[acyl carrier protein] synthase
(III, *Staphylococcus aureus*; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)
- IT 37278-30-1P, Acyl carrier protein synthase

(Staphylococcus aureus and Streptococcus pneumoniae; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

- IT 503876-73-1DP, subfragments and variants are claimed
503876-74-2DP, subfragments and variants are claimed
503876-75-3DP, subfragments and variants are claimed
503876-76-4DP, subfragments and variants are claimed
503876-77-5DP, subfragments and variants are claimed
503876-78-6DP, subfragments and variants are claimed
503876-79-7DP, subfragments and variants are claimed
503882-88-0DP, subfragments and variants are claimed
504444-78-4DP, Protein (Staphylococcus aureus gene obg),
subfragments and variants are claimed 504444-79-5DP, subfragments
and variants are claimed 504444-80-8DP, subfragments and variants
are claimed 504444-81-9DP, subfragments and variants are claimed
(amino acid sequence; cloning, purifn. and characterization of
polypeptides from pathogenic bacteria involved in
membrane biosynthesis, and drug screening and drug design
applications)
- IT 9014-24-8, RNA polymerase
(compn. contg. FtsZ protein and; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0,
Isopropanol, uses 77-92-9, Citric acid, uses 107-21-1, Ethylene
glycol, uses 107-41-5
(cryoprotectant; cloning, purifn. and characterization of
polypeptides from pathogenic bacteria involved in
membrane biosynthesis, and drug screening and drug design
applications)
- IT 110-82-7, Cyclohexane, uses 666-52-4, 2-Propanone-
1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6,
Chloroform-d 1076-43-3, Benzene-d6 1516-08-1,
Ethanol-d6 1665-00-5 1693-74-9 2037-26-5
2206-26-0, Acetonitrile-d3 2206-27-1
2679-89-2 4472-41-7, N,N-Dimethylformamide-d7
7291-22-7, Pyridine-d5 7789-20-0, Water-d2
17222-37-6
(deuterium lock solvent; cloning, purifn. and
characterization of **polypeptides** from pathogenic
bacteria involved in membrane biosynthesis, and drug screening
and drug design applications)
- IT 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9,
Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses
7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7,
Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium,

uses 7440-05-3, Palladium, uses 7440-06-4, Platinum, uses 7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses 7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9, Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium, uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses 7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4, Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses 7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1, Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses

(heavy atom label; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 1333-74-0, Hydrogen, uses 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses

(**isotope** label; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 3211-76-5, Selenomethionine
(label; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 25322-68-3, PEG
(low-mol.-wt., cryoprotectant; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs.
(**mass spectrometric** matrix; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 503876-65-1D, DNA (Staphylococcus aureus gene ftsZ), subfragments and variants are claimed 503876-66-2D, DNA (Staphylococcus aureus gene fabZ), subfragments and variants are claimed 503876-67-3D, DNA (Helicobacter pylori gene fabG), subfragments and variants are claimed 503876-68-4D, DNA (Staphylococcus aureus gene acpS), subfragments and variants are claimed 503876-69-5D, DNA

(*Helicobacter pylori* gene *murD*), subfragments and variants are claimed 503876-70-8D, DNA (*Helicobacter pylori* gene *murC*), subfragments and variants are claimed 503876-71-9D, DNA (*Staphylococcus aureus* gene *fabH*), subfragments and variants are claimed 503876-72-0D, DNA (*Staphylococcus aureus* gene *tagD*), subfragments and variants are claimed 504444-74-0D, DNA (*Staphylococcus aureus* gene *obg*), subfragments and variants are claimed 504444-75-1D, subfragments and variants are claimed 504444-76-2D, subfragments and variants are claimed 504444-77-3D, subfragments and variants are claimed

(nucleotide sequence; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 504489-14-9 504489-16-1 504489-17-2 504489-19-4 504489-21-8
504489-23-0 504489-24-1 504489-25-2 504489-29-6 504489-30-9

(unclaimed nucleotide sequence; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 504489-15-0 504489-18-3 504489-22-9
(unclaimed protein sequence; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

IT 503534-88-1 503882-57-3 503882-58-4 503882-59-5 503882-60-8
503882-61-9 503882-62-0 503882-63-1 503882-64-2 503882-65-3
503882-66-4 503882-67-5 503882-68-6 503882-69-7 503882-70-0
503882-71-1 503882-72-2 503882-73-3 503882-74-4 503882-75-5
503882-76-6 503882-77-7 503882-78-8 503882-79-9 503882-80-2
503882-81-3 503882-82-4 503882-83-5 503882-84-6 503882-85-7
503882-86-8 503882-87-9 503882-89-1 503882-90-4 504406-77-3
504406-78-4 504406-79-5 504406-80-8 504406-81-9 504406-82-0
504406-83-1 504406-84-2 504406-85-3 504406-86-4 504406-87-5
504406-88-6 504406-89-7 504406-90-0 504406-91-1 504406-92-2
504406-93-3 504406-94-4 504406-95-5 504406-96-6 504406-97-7
504410-35-9 504410-36-0 504410-37-1 504410-38-2 504410-39-3
504410-40-6 504410-41-7 504410-42-8 504410-43-9 504410-44-0
504410-45-1 504410-46-2 504410-47-3 504410-48-4 504410-49-5
504489-20-7

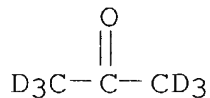
(unclaimed sequence; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in membrane biosynthesis, and drug screening and drug design applications)

acid processing and drug screening and drug design applications. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad Zahoor; Arrowsmith, Cheryl; Awrey, Donald; Beattie, Bryan; Canadien, Veronica; Cox, Brian; Domagala, Megan; Houston, Simon; Li, Qin; Nethery, Kathleen; Ng, Ivy; Ouyang, Hui; Pinder, Benjamin; Sheldrick, Bay; Viola, Cristina; Wrezel, Olga (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003025004 A2 20030327, 298 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-CA1411 20020918. PRIORITY: US 2001-PV323040 20010918; US 2001-PV325307 20010927; US 2001-PV325421 20010927; US 2001-PV325891 20010928; US 2001-PV326337 20011001; US 2001-PV326774 20011003; US 2001-PV327193 20011004; US 2001-PV340922 20011030; US 2001-PV338709 20011105; US 2001-PV333269 20011106; US 2001-PV341679 20011218.

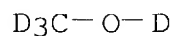
AB The present invention relates to **polypeptide** targets for pathogenic bacteria. A no. of antimicrobial target enzymes and **proteins** have been **identified**, expressed, and purified from *Staphylococcus aureus*, *Helicobacter pylori*, *Streptococcus pneumoniae*, and *Pseudomonas aeruginosa*. Cloning, the nucleotide sequences and the encoded amino acid sequences of genes *nrde*, *pyrH*, *pnpA*, *ung*, *rho*, *pnp*, *pyrE*, *lig*, *dnaN*, *nrde*, and *nrde* from *S. aureus*, *H. pylori*, *S. pneumoniae*, and *P. aeruginosa* are disclosed. The invention also provides biochem. and biophys. characteristics of those **polypeptides**. The **polypeptides** are characterized by using **mass spectrometry**, NMR, x-ray crystallog., and bioinformatics anal. The **polypeptides** of the invention can be used for drug screening, drug design, in diagnostic assays and in pharmacol. applications.

IT 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3,
Methanol-d4 865-49-6, Chloroform-d 1076-43-3,
Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5
1693-74-9 2037-26-5 2206-26-0,
Acetonitrile-d3 2206-27-1 2679-89-2
4472-41-7, N,N-Dimethylformamide-d7 7291-22-7,
Pyridine-d5 7789-20-0, Heavy water 17222-37-6
(deuterium lock solvent; cloning, purifn., sequences,
and characterization of **polypeptides** from pathogenic
bacteria involved in nucleic acid processing, and drug screening
and drug design applications)

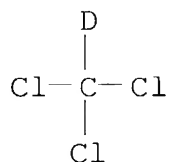
RN 666-52-4 HCA
CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



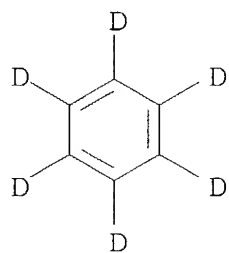
RN 811-98-3 HCA
CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



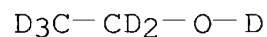
RN 865-49-6 HCA
CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



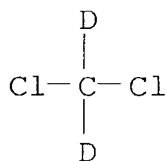
RN 1076-43-3 HCA
CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



RN 1516-08-1 HCA
CN Ethanol-d6 (9CI) (CA INDEX NAME)

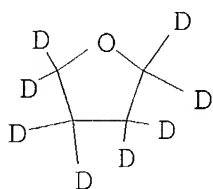


RN 1665-00-5 HCA
CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



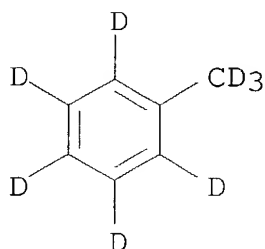
RN 1693-74-9 HCA

CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



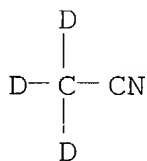
RN 2037-26-5 HCA

CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



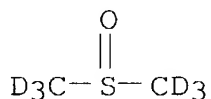
RN 2206-26-0 HCA

CN Acetonitrile-d3 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

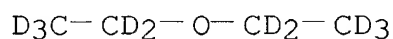


RN 2206-27-1 HCA

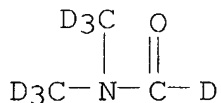
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



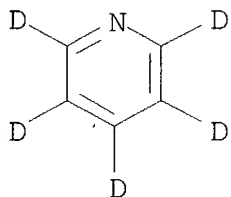
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



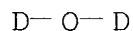
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



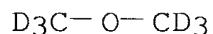
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IT 7782-39-0, Hydrogen-2, uses
 (isotope label; cloning, purifn., sequences, and
 characterization of **polypeptides** from pathogenic
 bacteria involved in nucleic acid processing, and drug screening
 and drug design applications)

RN 7782-39-0 HCA
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IC ICM C07K014-195
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 1, 6, 7, 10, 63
IT Proteins
(10,000-mol.-wt., compn. contg. uracil-DNA glycosylase and;
cloning, purifn., sequences, and characterization of
polypeptides from pathogenic bacteria involved in nucleic
acid processing, and drug screening and drug design applications)
IT Proteins
(25,000-mol.-wt., compn. contg. DNA ligase and; cloning, purifn.,
sequences, and characterization of **polypeptides** from
pathogenic bacteria involved in nucleic acid processing, and drug
screening and drug design applications)
IT Proteins
(88,000-mol.-wt., compn. contg. Rho factor and; cloning, purifn.,
sequences, and characterization of **polypeptides** from
pathogenic bacteria involved in nucleic acid processing, and drug
screening and drug design applications)
IT Enzymes, biological studies
(DNA gyrases, subunit A, compn. contg. or Rho factor and;
cloning, purifn., sequences, and characterization of
polypeptides from pathogenic bacteria involved in nucleic
acid processing, and drug screening and drug design applications)
IT Enzymes, biological studies
(DNA helicase, RuvA, compn. contg. uracil-DNA glycosylase and;
cloning, purifn., sequences, and characterization of
polypeptides from pathogenic bacteria involved in nucleic
acid processing, and drug screening and drug design applications)
IT Proteins
(FTSA, compn. contg. polynucleotide nucleotidyltransferase and;
cloning, purifn., sequences, and characterization of
polypeptides from pathogenic bacteria involved in nucleic
acid processing, and drug screening and drug design applications)
IT Molecular chaperones
(GroEL, compn. contg. uracil-DNA glycosylase and; cloning,
purifn., sequences, and characterization of **polypeptides**
from pathogenic bacteria involved in nucleic acid processing, and
drug screening and drug design applications)
IT Heat-shock proteins
(HSP 70, compn. contg. polynucleotide nucleotidyltransferase and;
cloning, purifn., sequences, and characterization of
polypeptides from pathogenic bacteria involved in nucleic

- acid processing, and drug screening and drug design applications)
- IT Ribosomal proteins
(L1, compn. contg. Rho factor and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Ribosomal proteins
(L6, compn. contg. uracil-DNA glycosylase and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Ribosomal proteins
(S4, compn. contg. ribonucleoside diphosphate reductase and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Infection
(bacterial; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Antibacterial agents
Bioinformatics
Cryoprotectants
Crystal growth
Crystal morphology
DNA sequences
Drug design
Drug screening
Exchange reaction
Gel electrophoresis
Helicobacter pylori
Mass spectrometry
Molecular cloning
NMR (nuclear magnetic resonance)
NMR spectroscopy
Pathogenic bacteria
Protein sequences
Pseudomonas aeruginosa
Solubility
Stability
Staphylococcus aureus
Streptococcus pneumoniae
X-ray diffractometry
(cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Fusion proteins (chimeric proteins)
(cloning, purifn., sequences, and characterization of

- polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Paraffin oils
(cryoprotectant; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(dnaN; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Elements
(heavy, label; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Molecular association
(**identification** of interacting **proteins**; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(lig; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT **Polyoxyalkylenes**, uses
(low-mol.-wt., cryoprotectant; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Epitopes
(mapping; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Proteins
(mutS, compn. contg. uracil-DNA glycosylase and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
Gene, microbial
(nrde; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(nrdf; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)

- IT Gene, microbial
(pnp; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(pnpA; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Organic compounds, biological studies
(**polypeptides** complexed with; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Conformation
(protein; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(pyrE; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(pyrH; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(rho; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Proteins
(single-stranded DNA-binding, compn. contg. uracil-DNA glycosylase and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Gene, microbial
(ung; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Genome
(virtual genome anal.; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT Transcription factors
(.rho., Staphylococcus aureus; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening

- and drug design applications)
- IT 9030-25-5P, Orotate phosphoribosyltransferase 9036-23-1P, Uridylate kinase
(*Helicobacter pylori*; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 9012-90-2 9068-08-0, Formate acetyltransferase
(*I*, compn. contg. Rho factor and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 59088-21-0P, Uracil DNA glycosylase
(*Pseudomonas aeruginosa*; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 9047-64-7P, Ribonucleoside diphosphate reductase
(*Staphylococcus aureus* and *S. pneumoniae*; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 9014-12-4P, Polyribonucleotide phosphorylase 455952-24-6P, DNA ligase
(*Staphylococcus aureus*; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 503638-31-1DP, subfragments and variants are claimed
503638-33-3DP, subfragments and variants are claimed
503638-35-5DP, subfragments and variants are claimed
503638-37-7DP, subfragments and variants are claimed
503638-39-9DP, subfragments and variants are claimed
503638-41-3DP, subfragments and variants are claimed
503638-43-5DP, subfragments and variants are claimed
503638-45-7DP, subfragments and variants are claimed
503638-47-9DP, subfragments and variants are claimed
503638-50-4DP, subfragments and variants are claimed
503638-51-5DP, subfragments and variants are claimed
(amino acid sequence; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 63363-78-0, Endonuclease IV
(compn. contg. DNA ligase and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)

- IT 9014-08-8, Enolase
(compn. contg. ribonucleoside diphosphate reductase major subunit and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and design applications)
- IT 9014-24-8, DNA-dependent RNA polymerase
(compn. contg. uracil-DNA glycosylase or Rho factor and; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 56-81-5, Glycerol, uses 64-18-6, Formic acid, uses 67-63-0, Isopropanol, uses 77-92-9, uses 107-21-1, Ethylene glycol, uses 107-41-5
(cryoprotectant; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 110-82-7, Cyclohexane, uses 666-52-4, 2-Propanone-1,1,1,3,3,3-d6 811-98-3, Methanol-d4 865-49-6, Chloroform-d 1076-43-3, Benzene-d6 1516-08-1, Ethanol-d6 1665-00-5 1693-74-9 2037-26-5 2206-26-0, Acetonitrile-d3 2206-27-1 2679-89-2 4472-41-7, N,N-Dimethylformamide-d7 7291-22-7, Pyridine-d5 7789-20-0, Heavy water 17222-37-6
(**deuterium** lock solvent; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 433935-36-5P, Polynucleotide nucleotidyl transferase
(homolog, Staphylococcus aureus; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 1333-74-0, Hydrogen, uses 7440-23-5, Sodium-23, uses 7723-14-0, Phosphorus-31, uses 7727-37-9, Nitrogen-14, uses 7782-39-0, Hydrogen-2, uses 7782-41-4, Fluorine-19, uses 10028-17-8, Hydrogen-3, uses 14390-96-6, Nitrogen-15, uses 14762-74-4, Carbon-13, uses
(**isotope** label; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)
- IT 3211-76-5, Selenomethionine 7429-91-6, Dysprosium, uses 7439-88-5, Iridium, uses 7439-90-9, Krypton, uses 7439-91-0, Lanthanum, uses 7439-92-1, Lead, uses 7439-94-3, Lutetium, uses 7439-97-6, Mercury, uses 7439-98-7, Molybdenum, uses 7440-00-8, Neodymium, uses 7440-04-2, Osmium, uses 7440-05-3, Palladium,

uses 7440-06-4, Platinum, uses 7440-10-0, Praseodymium, uses 7440-15-5, Rhenium, uses 7440-16-6, Rhodium, uses 7440-18-8, Ruthenium, uses 7440-19-9, Samarium, uses 7440-22-4, Silver, uses 7440-24-6, Strontium, uses 7440-25-7, Tantalum, uses 7440-27-9, Terbium, uses 7440-28-0, Thallium, uses 7440-29-1, Thorium, uses 7440-30-4, Thulium, uses 7440-31-5, Tin, uses 7440-33-7, Tungsten, uses 7440-39-3, Barium, uses 7440-43-9, Cadmium, uses 7440-45-1, Cerium, uses 7440-48-4, Cobalt, uses 7440-52-0, Erbium, uses 7440-53-1, Europium, uses 7440-54-2, Gadolinium, uses 7440-57-5, Gold, uses 7440-60-0, Holmium, uses 7440-61-1, Uranium, uses 7440-63-3, Xenon, uses 7440-64-4, Ytterbium, uses 7553-56-2, Iodine, uses 7726-95-6, Bromine, uses 7782-49-2, Selenium, uses

(label; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)

IT 25322-68-3, **Polyethylene glycol**

(low-mol.-wt., cryoprotectant; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)

IT 59-67-6D, Nicotinic acid, derivs. 621-82-9D, Cinnamic acid, derivs.

(**mass spectrometric** matrix; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)

IT 503638-30-0D, DNA (Staphylococcus aureus gene nrdE), subfragments and variants are claimed 503638-32-2D, DNA (Helicobacter pylori gene pyrH), subfragments and variants are claimed 503638-34-4D, DNA (Staphylococcus aureus gene pnpA), subfragments and variants are claimed 503638-36-6D, DNA (Pseudomonas aeruginosa gene ung), subfragments and variants are claimed 503638-38-8D, DNA (Staphylococcus aureus gene rho), subfragments and variants are claimed 503638-40-2D, subfragments and variants are claimed 503638-42-4D, DNA (Helicobacter pylori gene pyrE), subfragments and variants are claimed 503638-44-6D, DNA (Staphylococcus aureus gene lig), subfragments and variants are claimed 503638-46-8D, DNA (Staphylococcus aureus gene dnaN), subfragments and variants are claimed 503638-48-0D, DNA (Staphylococcus aureus gene nrdF), subfragments and variants are claimed 503638-49-1D, DNA (Streptococcus pneumoniae gene nrdE), subfragments and variants are claimed

(nucleotide sequence; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)

IT 1406-83-3, Leukocidin

(precursor, subunit F, compn. contg. ribonucleoside diphosphate reductase and; cloning, sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and design applications)

IT	503643-52-5	503643-54-7	503643-55-8	503643-57-0	503643-59-2
	503643-60-5	503643-61-6	503643-62-7	503643-63-8	503643-64-9
	503643-65-0	503643-67-2	503643-68-3	503643-69-4	503643-71-8
	503643-72-9	503643-73-0	503643-75-2	503643-76-3	503643-78-5
	503643-80-9	503643-81-0	503643-82-1	503643-84-3	503643-85-4
	503643-86-5	503643-88-7	503643-89-8	503643-90-1	503643-92-3
	503643-93-4				

(unclaimed nucleotide sequence; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing and drug screening and drug design applications)

IT	503643-53-6	503643-56-9	503643-58-1	503643-66-1	503643-70-7
	503643-74-1	503643-77-4	503643-79-6	503643-83-2	503643-87-6
	503643-91-2				

(unclaimed protein sequence; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing and drug screening and drug design applications)

IT	503607-95-2	503607-96-3	503607-97-4	503607-98-5	503607-99-6
	503608-00-2	503608-01-3	503608-02-4	503608-03-5	503608-04-6
	503608-05-7	503608-06-8	503608-07-9	503608-08-0	503608-09-1
	503608-10-4	503608-11-5	503608-12-6	503608-13-7	503608-14-8
	503608-15-9	503608-16-0	503608-17-1	503608-18-2	503608-19-3
	503608-20-6	503608-21-7	503608-22-8	503608-23-9	503608-24-0
	503608-25-1	503608-26-2	503608-27-3	503608-28-4	503608-29-5
	503608-30-8	503608-31-9	503608-32-0	503608-33-1	503608-34-2
	503608-35-3	503608-36-4	503608-37-5	503608-38-6	503608-39-7
	503608-40-0	503608-41-1	503608-42-2	503608-43-3	503608-44-4
	503608-45-5	503608-46-6	503608-47-7	503608-48-8	503608-49-9
	503608-50-2	503608-51-3	503608-52-4	503608-53-5	503608-54-6
	503608-55-7	503608-56-8	503608-57-9	503608-58-0	503608-59-1
	503608-60-4	503608-61-5	503608-62-6	503608-64-8	503608-66-0
	503608-67-1	503608-68-2	503608-69-3	503608-70-6	503608-71-7
	503608-72-8	503608-73-9	503608-74-0	503608-75-1	503608-76-2
	503608-77-3	503608-78-4	503608-79-5	503608-80-8	503608-81-9
	503608-82-0	503608-83-1	503608-84-2	503608-85-3	503608-86-4
	503608-87-5	503608-88-6	503608-89-7	503608-90-0	503608-91-1
	503608-92-2	503608-93-3	503608-94-4	503608-95-5	503608-96-6
	503608-97-7	503608-98-8	503608-99-9	503609-00-5	503609-01-6
	503609-02-7	503609-03-8	503609-04-9	503609-05-0	503609-06-1

(unclaimed sequence; cloning, purifn. and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing and drug screening and drug design applications)

IT	37217-33-7P, DNA polymerase III
----	---------------------------------

(.beta.-subunit, Staphylococcus aureus; cloning, purifn., sequences, and characterization of **polypeptides** from pathogenic bacteria involved in nucleic acid processing, and drug screening and drug design applications)

L101 ANSWER 18 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:267686 Purification of enzymes involved in coenzyme metabolism from pathogenic bacteria for characterization in development of targets for antibiotics. Edwards, Aled; Dharamsi, Akil; Vedadi, Masoud; Alam, Muhammad Zahoor; Awrey, Donald; Beattie, Bryan; Canadien, Veronica; Domagala, Megan; Houston, Simon; Kanagarajah, Dhushy; Li, Qin; Necakov, Sasha; Nethery, Kathleen; Pinder, Benjamin; Sheldrick, Bay; Vallee, Francois; Viola, Cristina (Affinium Pharmaceuticals, Inc., Can.). PCT Int. Appl. WO 2003025006 A2 20030327, 256 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2002-CA1427 20020920. PRIORITY: US 2001-PV324115 20010921; US 2001-PV325337 20010927; US 2001-PV326321 20011001; US 2001-PV326378 20011001; US 2001-PV326820 20011003; US 2001-PV335702 20011025; US 2001-PV340536 20011026; US 2001-PV350907 20011029.

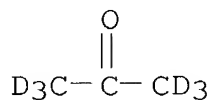
AB Methods of purifying and characterizing enzymes that may play a role in cofactor metab. in pathogenic bacteria are described. The proteins may be useful as targets for antibiotics and methods for identifying regions of the proteins that may be targeted by drugs are described. The invention also provides biochem. and biophys. characteristics of those **polypeptides**.

IT 666-52-4, Perdeuteroacetone 811-98-3, Methanol-d4
865-49-6, Deuteriochloroform 1076-43-3,
Perdeuterobenzene 1516-08-1, Ethanol-d6 1665-00-5
1693-74-9, Perdeuterotetrahydrofuran 2037-26-5
2206-26-0, Perdeuteroacetonitrile 2206-27-1,
Dimethylsulfoxide-d6 2679-89-2, Diethyl ether-d10
4472-41-7, N,N-Dimethylformamide-d7 7291-22-7,
Pyridine-d5 7789-20-0, Heavy water 17222-37-6

(as **deuterium** lock solvent in NMR of proteins; purifn.
of enzymes involved in coenzyme metab. from pathogenic bacteria
for characterization in development of targets for antibiotics)

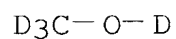
RN 666-52-4 HCA

CN 2-Propanone-1,1,1,3,3,3-d6 (9CI) (CA INDEX NAME)



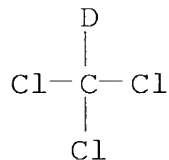
RN 811-98-3 HCA

CN Methanol-d4 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



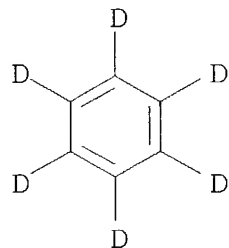
RN 865-49-6 HCA

CN Methane-d, trichloro- (9CI) (CA INDEX NAME)



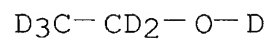
RN 1076-43-3 HCA

CN Benzene-d6 (8CI, 9CI) (CA INDEX NAME)



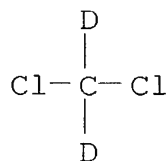
RN 1516-08-1 HCA

CN Ethanol-d6 (9CI) (CA INDEX NAME)



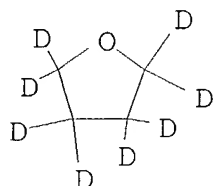
RN 1665-00-5 HCA

CN Methane-d2, dichloro- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



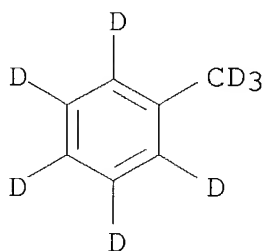
RN 1693-74-9 HCA

CN Furan-d4, tetrahydro-d4- (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



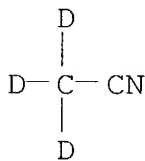
RN 2037-26-5 HCA

CN Benzene-d5, methyl-d3- (9CI) (CA INDEX NAME)



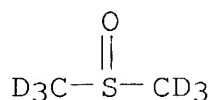
RN 2206-26-0 HCA

CN Acetonitrile-d3 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)

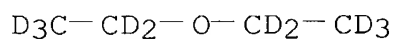


RN 2206-27-1 HCA

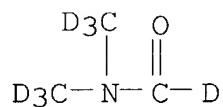
CN Methane-d3, sulfinylbis- (9CI) (CA INDEX NAME)



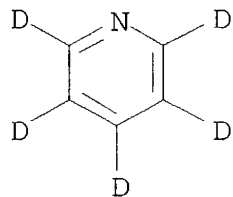
RN 2679-89-2 HCA
 CN Ethane-d5, 2,2'-oxybis- (9CI) (CA INDEX NAME)



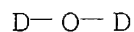
RN 4472-41-7 HCA
 CN Formamide-1-d, N,N-di(methyl-d3)- (7CI, 8CI, 9CI) (CA INDEX NAME)



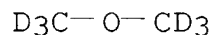
RN 7291-22-7 HCA
 CN Pyridine-d5 (6CI, 7CI, 8CI, 9CI) (CA INDEX NAME)



RN 7789-20-0 HCA
 CN Water-d2 (9CI) (CA INDEX NAME)



RN 17222-37-6 HCA
 CN Methane-d3, oxybis- (9CI) (CA INDEX NAME)



IT 7782-39-0, Deuterium, biological studies
 (as isotopic label for NMR of proteins; purifn. of
 enzymes involved in coenzyme metab. from pathogenic bacteria for
 characterization in development of targets for antibiotics)
 RN 7782-39-0 HCA

CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IC ICM C07K014-195

CC 7-2 (Enzymes)

Section cross-reference(s): 1, 3, 6, 16

ST enzyme purifn NMR **mass spectrometry** genomics;
coenzyme biosynthesis enzyme antibiotic design selection

IT Hydrocarbon oils

Polyoxyalkylenes, biological studies

(as cryoprotectant; purifn. of enzymes involved in coenzyme
metab. from pathogenic bacteria for characterization in
development of targets for antibiotics)

IT NMR spectroscopy

(**deuterium**; purifn. of enzymes involved in coenzyme
metab. from pathogenic bacteria for characterization in
development of targets for antibiotics)

IT Crystallization

Mass spectrometry

(of **proteins**; purifn. of enzymes involved in coenzyme
metab. from pathogenic bacteria for characterization in
development of targets for antibiotics)

IT 56-81-5, Glycerol, biological studies 64-18-6, Formic acid,
biological studies 67-63-0, Isopropanol, biological studies
77-92-9, Citric acid, biological studies 107-21-1, Ethylene
glycol, biological studies 5683-44-3, 3-Methyl-2,4-pentanediol
25322-68-3, **Polyethylene glycol**

(as cryoprotectant; purifn. of enzymes involved in coenzyme
metab. from pathogenic bacteria for characterization in
development of targets for antibiotics)

IT 110-82-7, Cyclohexane, analysis **666-52-4**,
Perdeuteroacetone **811-98-3**, Methanol-d4 **865-49-6**
, Deuteriochloroform **1076-43-3**, Perdeuterobenzene
1516-08-1, Ethanol-d6 **1665-00-5** **1693-74-9**
, Perdeuterotetrahydrofuran **2037-26-5** **2206-26-0**,
Perdeuteroacetonitrile **2206-27-1**, Dimethylsulfoxide-d6
2679-89-2, Diethyl ether-d10 **4472-41-7**,
N,N-Dimethylformamide-d7 **7291-22-7**, Pyridine-d5
7789-20-0, Heavy water **17222-37-6**

(as **deuterium** lock solvent in NMR of proteins; purifn.
of enzymes involved in coenzyme metab. from pathogenic bacteria
for characterization in development of targets for antibiotics)

IT 1333-74-0, Hydrogen, biological studies 7440-23-5, Sodium-23,
biological studies 7723-14-0, Phosphorus-31, biological studies
7727-37-9, Nitrogen 14, biological studies **7782-39-0**,
Deuterium, biological studies 7782-41-4, Fluorine-19,

biological studies 10028-17-8, Tritium, biological studies
14390-96-6, Nitrogen 15, biological studies 14762-74-4, Carbon 13,
biological studies

(as **isotopic** label for NMR of proteins; purifn. of
enzymes involved in coenzyme metab. from pathogenic bacteria for
characterization in development of targets for antibiotics)

L101 ANSWER 19 OF 28 HCA COPYRIGHT 2004 ACS on STN

138:182010 Nucleic acid sensor molecules comprising target modulation
domains and catalytic domains with an optical signal generating
unit. Stanton, Martin; Epstein, David; Hamaguchi, Nobuko; Kurz,
Markus; Keefe, Tony; Wilson, Charles; Grate, Dilara; Marshall,
Kristin A.; McCauley, Thomas; Kurz, Jeffrey (Archemix Corp., USA).
PCT Int. Appl. WO 2003014375 A2 20030220, 424 pp. DESIGNATED
STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA,
CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE,
GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL,
PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG,
US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW:
AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB,
GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR.
(English). CODEN: PIXXD2. APPLICATION: WO 2002-US25319 20020809.
PRIORITY: US 2001-PV311378 20010809; US 2001-PV313932 20010821; US
2001-952680 20010913; US 2001-PV338186 20011113; US 2002-PV349959
20020118; US 2002-PV364486 20020313; US 2002-PV367991 20020325; US
2002-PV369887 20020404; US 2002-PV376744 20020501; US 2002-PV385097
20020531.

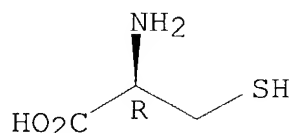
AB Methods for engineering a nucleic acid sensor mol. (also known as
allosteric ribozymes, aptazymes, and the like) are provided.
Biosensors comprise a plurality of nucleic acid sensor mols. labeled
with a first signaling moiety and a second signaling moiety. The
nucleic acid sensor mols. recognizes target mols. which do not
naturally bind to DNA. Binding of a target mol. to the sensor mols.
triggers a change in the proximity of the signaling moieties which
leads to a change in the optical properties of the nucleic acid
sensor mols. on the biosensor. The nucleic acid sensor mols. are
developed through a combination of engineering and selection methods
that are useful for identifying nucleic acid sensor mols. against a
wide variety of target mols. including protein (including specific
post-translationally modified forms of proteins), **peptides**
, nucleic acids, oligosaccharides, nucleotides, metabolites, drugs,
toxins, biohazards, ions, carbohydrates, glycoproteins, hormones,
receptors, antibodies, viruses, transition state analogs, cofactors,
dyes, growth factors, nutrients, etc. The selection process
identified novel sensor mols. through target modulation of the
catalytic core of a ribozyme. Hence, in vitro selection is distinct
from previously described for affinity-based aptamer selections

(e.g., SELEX) in that selective pressure on the starting population of nucleic acid sensors results in mols. with enhanced catalytic properties, but not in enhanced binding properties. In one embodiment of the invention, nucleic acid sensors are based on cis-cleaving hammerhead ribozymes that have been designed to work as optical signaling mols. affixed to a solid support, and utilize fluorescence and FRET-based methods of signal generation and detection. The method is useful in diagnostic applications and drug optimization.

IT 52-90-4, L-Cysteine, biological studies
(acylation, **detection of proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

RN 52-90-4 HCA
CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



IC ICM C12Q
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 1, 7, 9

IT **Proteins**
(GTP-binding, **detection of**; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Phosphatidylinositols
(addn. of, **detection of proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Alkylation
(biochem., **detection of proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Acetylation
Acylation
Glycosylation
(biol., **detection of proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Deamination
(biol., of asparagine, **detection of proteins**

modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Carboxylation

(biol., of glutamine, **detection of proteins**

modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Hydroxylation

(biol., of proline, **detection of proteins**

modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Myristoylation

Prenylation

(**detection of proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Lipids, biological studies

(**detection of proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Cytokines

Estrogen receptors

G **protein**-coupled receptors

G proteins (guanine nucleotide-binding **proteins**)

(**detection of**; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Disulfide group

(formation, **detection of proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Biosensors

Blood analysis

Drug screening

Drugs

Dyes

Fluorescence

Fluorescence quenching

Fluorescence resonance energy transfer

Fluorescent indicators

High throughput screening

Ions

Isotope indicators

Nucleic acid hybridization

Nutrients

Surface plasmon resonance

Virus

(nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Antibodies

Antigens

Carbohydrates, analysis

Coenzymes

Growth factors, animal

Hormones, animal, analysis

Nucleotides, analysis

Oligosaccharides, analysis

Peptides, analysis

Polysaccharides, analysis

Proteins

Receptors

Toxins

(nucleic acid **sensor** mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT Phosphorylation, biological

(**protein**, **detection of proteins**

modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT 147-85-3, L-Proline, biological studies

(4-hydroxylation, **detection of proteins**

modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT 52-90-4, L-Cysteine, biological studies

(acylation, **detection of proteins** modified

by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT 56-85-9, L-Glutamine, biological studies

(carboxylation and deamination, **detection of**

proteins modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT 70-47-3, L-Asparagine, biological studies

(deamination, **detection of proteins** modified

by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)

IT 60-92-4, CAMP 3616-08-8, CCMP 7665-99-8, CGMP 9001-63-2,

Lysozyme 9013-05-2, Phosphatase 9036-21-9, CAMP

phosphodiesterase 9068-52-4, CGMP phosphodiesterase 103171-49-9,

- Ras kinase 137632-07-6, ERK1 kinase 137632-08-7, ERK2 kinase 139691-76-2, RAF kinase 142243-02-5, ERK kinase 142243-02-5D, ERK kinase, phosphorylated 142805-58-1, Mitogen-activated **protein** kinase kinase 146702-84-3D, MEK kinase, phosphorylated 155215-87-5, JNK kinase 165245-96-5, p38 MAP kinase 372092-80-3, **Protein** kinase
(**detection** of; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)
- IT 10028-17-8, Tritium, uses 14158-31-7, Iodine-125, uses 14596-37-3, Phosphorus-32, uses 14762-75-5, Carbon-14, uses 15117-53-0, Sulfur-35, uses 15749-66-3, Phosphorus-33, uses
(**radioactive label** for sensor; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)
- IT 63-68-3, L-Methionine, biological studies
(removal of, **detection** of **proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)
- IT 60267-61-0, Ubiquitin
(ubiquitination, **detection** of **proteins** modified by; nucleic acid sensor mols. comprising target modulation domains and catalytic domains with an optical signal generating unit)
- L101 ANSWER 20 OF 28 HCA COPYRIGHT 2004 ACS on STN
137:197868 Phosphoprotein binding agents and methods of their use. Goshe, Michael B.; Conrads, Thomas P.; Veenstra, Timothy D.; Panisko, Ellen A. (USA). U.S. Pat. Appl. Publ. US 2002119505 A1 20020829, 20 pp. (English). CODEN: USXXCO. APPLICATION: US 2001-788286 20010216.
- AB The invention provides reagents and methods for characterizing (i.e., identification and/or quantitation) the phosphorylation states of proteins. Proteins may be post-transcriptionally modified such that they contain phosphate groups at either some or all of their serine, threonine, tyrosine, histidine, and/or lysine amino acid residues. In many cases the extent to which a **protein** is phosphorylated **dets.** its bioactivity, i.e., its ability to effect cell functions such as differentiation, division, and metab. Hence, a powerful tool for diagnosing various diseases and for furthering the understanding of protein-protein interactions is provided. Two equal .beta.-casein samples were labeled with ethanedithiol (EDT) or EDT-2H4, resp., under .beta.-elimination conditions with NaOH. The labeled samples were quenched, desalted, denatured, reduced, biotinylated with iodoacetyl-**PEO**-biotin, and **digested** with trypsin. The labeled **peptides** were purified by affinity chromatog. using

immobilized avidin and analyzed capillary reversed-phase liq.
chromatog.-**mass spectrometry**.

IT 7782-39-0, 2H, uses
(as label; phosphoprotein binding agents and methods of use)
RN 7782-39-0 HCA
CN Deuterium (7CI, 8CI, 9CI) (CA INDEX NAME)

D-D

IT 100189-81-9, 1,2-Ethane-1,1,2,2-d4-dithiol
(phosphoprotein binding agents and methods of use)
RN 100189-81-9 HCA
CN 1,2-Ethane-1,1,2,2-d4-dithiol (9CI) (CA INDEX NAME)

HS- CD2- CD2- SH

IC ICM G01N033-537
ICS G01N033-543
NCL 435007920
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 6
ST phosphoprotein phosphorylation analysis reagent; diagnosis
phosphoprotein binding agent; protein interaction study
phosphoprotein binding agent; beta casein phosphopeptide labeling
deuterated ethandithiol; affinity chromatog **mass**
spectrometry phosphopeptide identification
IT **Isotopes**
(as labels; phosphoprotein binding agents and methods of use)
IT **Protein sequence analysis**
(**mass spectrometric**; phosphoprotein binding
agents and methods of use)
IT Amino acids, **analysis**
(phosphates, **protein** contg.; phosphoprotein binding
agents and methods of use)
IT Affinity chromatography
Cell
Cell differentiation
Cell division
Chromatography
Coupling agents
Diagnosis
Disease, animal
Metabolism
Metabolism, animal
Phosphate group
Samples

- Tandem **mass spectrometry**
(phosphoprotein binding agents and methods of use)
- IT **Peptides**, analysis
(phosphoprotein binding agents and methods of use)
- IT **Mass spectrometry**
(**protein sequence anal.**; phosphoprotein
binding agents and methods of use)
- IT 7782-39-0, 2H, uses 13965-97-4, 34S, uses 13968-48-4,
170, uses 14390-96-6, 15N, uses 14762-74-4, 13C, uses
14797-71-8, 18O, uses
(as label; phosphoprotein binding agents and methods of use)
- IT 540-63-6, 1,2-Ethanedithiol **100189-81-9**,
1,2-Ethane-1,1,2,2-d4-dithiol 339082-21-2
(phosphoprotein binding agents and methods of use)

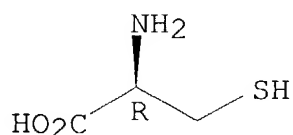
L101 ANSWER 21 OF 28 HCA COPYRIGHT 2004 ACS on STN

136:366141 Method for **assaying protein**

nitrosylation. Jaffrey, Samie; Ferris, Christopher D.; Snyder, Solomon H. (The Johns Hopkins University, USA; Memorial Sloan-Kettering Cancer Center; Erdjument-Bromage, Hediye; Tempst, Paul). PCT Int. Appl. WO 2002039119 A2 20020516, 39 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2001-US42826 20011029. PRIORITY: US 2000-PV244097 20001027.

- AB Many of the effects of nitric oxide are mediated by the direct modification of **cysteine** residues resulting in an adduct called a nitrosothiol. A method to **detect proteins** which contain nitrosothiols involves several steps. Nitrosylated **cysteines** are converted to tagged **cysteines**. Tagged proteins can then be detected, for example, by immunoblotting and/or can be purified by affinity chromatog. The method is applicable to the detection of S-nitrosylated proteins in cell lysates following in vitro S-nitrosylation, as well as to the detection of endogenous S-nitrosothiols in selected protein substrates.
- IT **52-90-4, L-Cysteine**, biological studies
(method for **assaying protein** nitrosylation)
- RN 52-90-4 HCA
- CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



- IC ICM G01N033-68
- CC 9-14 (Biochemical Methods)
Section cross-reference(s): 6
- ST **protein nitrosylation assay** nitrosothiol
- IT Heat-shock proteins
(HSP 72; method for **assaying protein**
nitrosylation)
- IT Neurofilament proteins
(NF-H; method for **assaying protein**
nitrosylation)
- IT Glutamate receptors
(NMDA-binding, NR1 or NR2 subunits; method for **assaying**
protein nitrosylation)
- IT Transcription factors
(Rb; method for **assaying protein**
nitrosylation)
- IT **Radioactive** substances
(as label on activated mixed **disulfide**;
method for **assaying protein nitrosylation**)
- IT **Peptides**, biological studies
(as label on activated mixed **disulfide**; method for
assaying protein nitrosylation)
- IT Proteins
(collapsin response mediator protein 1; method for
assaying protein nitrosylation)
- IT Proteins
(collapsin response mediator protein 2; method for
assaying protein nitrosylation)
- IT Proteins
(collapsin response mediator protein 4; method for
assaying protein nitrosylation)
- IT **Disulfides**
(detectably tagged and activated mixed; method for
assaying protein nitrosylation)
- IT Drug screening
(for drugs modulating protein nitrosylation; method for
assaying protein nitrosylation)
- IT Cation channel
(hyperpolarization-activated, isoform 2 or 3 of; method for
assaying protein nitrosylation)
- IT Immunoassay

- (immunoblotting; method for **assaying protein nitrosylation**)
- IT Affinity chromatography
- Nitrosation
- Test kits
 - (method for **assaying protein nitrosylation**)
- IT Antibodies
- Avidins
 - (method for **assaying protein nitrosylation**)
- IT Calbindins
 - (method for **assaying protein nitrosylation**)
- IT Thiols (organic), biological studies
 - (method for **assaying protein nitrosylation**)
- IT Proteins
 - (nitrosylated; method for **assaying protein nitrosylation**)
- IT Blood vessel
- Brain
- Macrophage
 - (test sample from; method for **assaying protein nitrosylation**)
- IT Nitrosation
 - (thionitrosation; method for **assaying protein nitrosylation**)
- IT Tubulins
 - (.alpha.-; method for **assaying protein nitrosylation**)
- IT Actins
- Tubulins
 - (.beta.-; method for **assaying protein nitrosylation**)
- IT Actins
 - (.gamma.-; method for **assaying protein nitrosylation**)
- IT 58-85-5, Biotin 25550-58-7, Dinitrophenol
 - (as label on activated mixed **disulfide**; method for **assaying protein nitrosylation**)
- IT 125978-95-2, Nitric oxide synthetase
 - (endothelial and neuronal; method for **assaying protein nitrosylation**)
- IT 9001-51-8, Hexokinase
 - (isoform 1; method for **assaying protein nitrosylation**)
- IT 9013-20-1, Streptavidin
 - (method for **assaying protein nitrosylation**)
- IT 9001-15-4, Creatine kinase 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase 9035-74-9, Glycogen phosphorylase
 - (method for **assaying protein nitrosylation**)

Wallenhorst 10/045,170

- IT 52-90-4, L-Cysteine, biological studies
(method for **assaying protein** nitrosylation)
- IT 50-81-7, L-Ascorbic acid, uses 67-64-1, Acetone, uses 134-0
Sodium ascorbate 151-21-3, SDS, uses
(method for **assaying protein** nitrosylation)
- IT 2949-92-0 3614-08-2, **Selenocysteine** 15537-71-0,
N-Acetylpenicillamine 67776-06-1, S-Nitrosoacetylpenicillamine
129179-83-5
(method for **assaying protein** nitrosylation)
- IT 9000-83-3
(potassium-sodium-dependent, .alpha.1 or .alpha.2 subunit; method
for **assaying protein** nitrosylation)

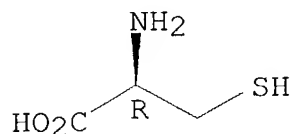
L101 ANSWER 22 OF 28 HCA COPYRIGHT 2004 ACS on STN

134:307611 Conjugated polymer tag complexes and their preparation and
use in assays. Leif, Robert C.; Franson, Richard C.; Vallarino,
Lidia (USA). PCT Int. Appl. WO 2001027625 A1 20010419, 104 pp.
DESIGNATED STATES: W: CA, CH, DE, FI, GB, JP, US; RW: AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE.
(English). CODEN: PIXXD2. APPLICATION: WO 2000-US27787 20001007.
PRIORITY: US 1999-PV158718 19991008.

AB Processes are described for: (1) the sequential solid phase
synthesis of polymers with at least one tag, which can be a light
emitting and/or absorbing mol. species (optical-label), a
paramagnetic or **radioactive label**, or a tag that
permits the phys. sepn. of particles including cells. When multiple
optical-labels are suitably arranged in three-dimensional space, the
energy transfer from one mol. species to another can be maximized
and the radiationless loss between members of the same mol. species
can be minimized; (2) the coupling of these polymers to biol. active
and/or biol. compatible mols. through peripheral pendant
substituents having at least one reactive site; and (3) the specific
cleavage of the coupled polymer from a solid phase support. The
tagged-**peptide** or polymers produced by these processes and
their conjugates with an analyte-binding species, such as a
monoclonal antibody or a polynucleotide probe are described. When
functionalized europium macrocyclic complexes, as taught in our U.S.
patents 5,373,093 and 5,696,240, are bound to polylysine and other
peptides, the emitted light increases linearly with the amt.
of bound macrocyclic complex. Similar linearity will also result
for multiple luminescent macrocyclic complexes of other lanthanide
ions, such as samarium, terbium, and dysprosium, when they are bound
to a polymer or mol.

- IT 52-90-4, L-Cysteine, biological studies
(conjugated polymer tag complexes and prepn. and use in assays)
- RN 52-90-4 HCA
- CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



- IC ICM G01N033-545
- ICS G01N033-543; G01N033-576; G01N033-532; C08F002-10; C08F002-50;
C08F290-14
- CC 9-15 (Biochemical Methods)
Section cross-reference(s): 2, 6, 34, 78, 79, 80
- ST conjugated polymer tag prepn assay reagent **peptide**
- IT Paramagnetic materials
 - Radioactive** substances
(as **labels**; conjugated polymer tag complexes and prepn.
and use in assays)
- IT Amino group
- Apoptosis
- Azo dyes
- B cell (lymphocyte)
- Bacillus stearothermophilus
- Carboxyl group
- Cell cycle
- Centromeres
- Chromosome
- Combinatorial chemistry
- Conformation
- Cyanine dyes
- Cyano group
- Disulfide** group
- Drugs
- Drugs of abuse
- Energy transfer
- Fluorescent indicators
- Fluorescent substances
- Formyl group
- Human immunodeficiency virus
- Human immunodeficiency virus 1
- Hydroxyl group
- Leukocyte
- Luminescence
- Neoplasm
- Nocardia otitidiscaviarum
- Nucleic acid hybridization
- Nucleosome
- Optical absorption

Pesticides
Reducing agents
Ribosome
Solid phase synthesis
Stains, biological
Sulfhydryl group
T cell (lymphocyte)
Telomeres (chromosome)
pH
 (conjugated polymer tag complexes and prepn. and use in assays)
IT Agglutinins and Lectins
Albumins, analysis
Antigens
Avidins
Blood-group substances
CD20 (antigen)
CD4 (antigen)
CD8 (antigen)
Carcinoembryonic antigen
Collagens, analysis
Cyclins
DNA
Ecdysteroids
Estrogen receptors
Estrogens
Globulins, analysis
Glucocorticoid receptors
Glycoproteins, general, analysis
Glycosaminoglycans, analysis
Hemoglobins
Hormone receptors
Hormones, animal, analysis
Immunoglobulins
Keratins
Lymphokines
Nucleic acids
Nucleosides, analysis
P-glycoproteins
 Peptides, analysis
Polynucleotides
Polysaccharides, analysis
Progesterone receptors
Proliferating cell nuclear antigen
Prostaglandins
 Proteins, general, analysis
RNA
Toxins
Viral RNA

Vitamins
mRNA
neu (receptor)
p53 (protein)
.alpha.-Fetoproteins
(conjugated polymer tag complexes and prepn. and use in assays)
IT Nucleic acids
 Peptides, preparation
Polymers, preparation
(conjugates; conjugated polymer tag complexes and prepn. and use
in assays)
IT **Peptides**, analysis
Steroids, analysis
(hormones; conjugated polymer tag complexes and prepn. and use in
assays)
IT **52-90-4, L-Cysteine**, biological studies 73-22-3,
L-Tryptophan, biological studies 38240-29-8 142939-57-9
335196-03-7
(conjugated polymer tag complexes and prepn. and use in assays)

L101 ANSWER 23 OF 28 HCA COPYRIGHT 2004 ACS on STN

119:155015 Protein- and **peptide**-metal ion complexes for
disease diagnosis and therapy. Rhodes, Buck A.; Zamora, Paul O.
(Rhomed Inc., USA). PCT Int. Appl. WO 9312819 A1 19930708, 61 pp.
DESIGNATED STATES: W: AT, AU, BB, BG, BR, CA, CH, CS, DE, DK, ES,
FI, GB, HU, JP, KP, KR, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO,
RU, SD, SE; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR,
GA, GB, GR, IE, IT, LU, MC, ML, MR, NL, PT, SE, SN, TD, TG.
(English). CODEN: PIXXD2. APPLICATION: WO 1992-US11334 19921231.
PRIORITY: US 1992-816476 19920103; US 1992-816477 19920103; US
1992-840077 19920220; US 1992-998820 19921230; US 1992-998910
19921230.

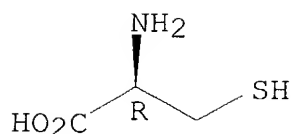
AB The title metal/proteins or **peptides** complexes comprise a
biol. function domain (e.g. IKVAV or YIGSR-contg. domain), a metal
ion-binding domain (e.g. domain contg. S, N, O, **cysteine**,
penicillamide), and a metal ion label (Fe, Co, Ni, etc.). Thus,
99mTc-labeled H2N-Cys-Asp-Pro-Gly-Tyr-Ile-Gly-Ser-Arg was prepd. by
reaction with stannous tartrate, and then **radiolabeling**
with Na99mTcO4. The labeled **peptide** was used for
detecting clots.

IT **52-90-4, Cysteine**, biological studies
(protein or **peptide** with metal ion-binding domain
contg., metal ion complexed with, for disease diagnosis or
therapy)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



- IC ICM A61K049-02
ICS A61K043-00; C07K007-00; C07K015-28
- CC 8-9 (Radiation Biochemistry)
- ST metal protein complex imaging agent; **peptide** metal complex
imaging agent; clot imaging protein metal complex; therapeutic
polypeptide metal complex
- IT Abscess
(**detection** of occult, **protein/peptide**
-metal ion complexes for)
- IT Emphysema
Inflammation
Thrombus and Blood clot
(**detection** of, **protein/peptide**
-metal ion complexes for)
- IT Imaging
(NMR, **protein/peptide**-metal complexes for)
- IT Intestine, neoplasm
(colon, carcinoma, **detection** of, **protein/**
peptide-metal ion complexes for)
- IT Proteins, specific or class
(**disulfide**-contg., labeling of, by redn./complex
formation with stannous ion, for disease diagnosis and therapy)
- IT Tomography
(gamma-ray, **protein/peptide**-metal complexes for)
- IT Lung, neoplasm
(melanoma, **detection** of, **protein/**
peptide-metal ion complexes for)
- IT **Peptides**, compounds
(metal complexes, prepn. of, for disease diagnosis and therapy)
- IT Tomography
(positron-emission, computerized, **protein/peptide**-metal
complexes for)
- IT Tomography
(single-photon-emission, computerized, **protein/peptide**
-metal complexes for)
- IT 22541-90-8, Tin(2+), biological studies
(agent contg., for redn./complex formation with thiolate-contg.
protein, for disease **diagnosis** and therapy)
- IT 7439-88-5D, Iridium, biol. function domain-contg. and metal
ion-binding domain-contg. protein or **peptide** complexes
- 7439-89-6D, Iron, biol. function domain-contg. and metal ion-binding

domain-contg. protein or **peptide** complexes 7439-92-1D,
Lead, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7439-97-6D,
Mercury, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7439-98-7D,
Molybdenum, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-02-0D,
Nickel, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-04-2D,
Osmium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-05-3D,
Palladium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-06-4D,
Platinum, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-08-6D,
Polonium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-15-5D,
Rhenium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-18-8D,
Ruthenium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-22-4D,
Silver, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-26-8D,
Technetium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-28-0D,
Thallium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-36-0D,
Antimony, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-38-2D,
Arsenic, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-43-9D,
Cadmium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-48-4D,
Cobalt, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-50-8D,
Copper, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-57-5D,
Gold, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-66-6D,
Zinc, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-68-8D,
Astatine, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-69-9D,
Bismuth, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7440-74-6D,
Indium, biol. function domain-contg. and metal ion-binding
domain-contg. protein or **peptide** complexes 7782-49-2D,
Selenium, biol. function domain-contg. and metal ion-binding

- domain-contg. protein or **peptide** complexes
(for disease diagnosis and therapy)
- IT 110590-64-2 131167-89-0
(protein or **peptide** contg. biol. function domain
fragment of, metal ion complexed with, for disease diagnosis or
therapy)
- IT 52-67-5, Penicillamine 52-90-4, **Cysteine**,
biological studies 56-84-8, Aspartic acid, biological studies
56-86-0, Glutamic acid, biological studies 56-87-1, Lysine,
biological studies 56-89-3, Cystine, biological studies 60-18-4,
Tyrosine, biological studies 63-68-3D, Methionine, deacylated
71-00-1, Histidine, biological studies 74-79-3, Arginine,
biological studies 7704-34-9, Sulfur, biological studies
7727-37-9, Nitrogen, biological studies 7782-44-7, Oxygen,
biological studies
(protein or **peptide** with metal ion-binding domain
contg., metal ion complexed with, for disease diagnosis or
therapy)
- L101 ANSWER 24 OF 28 HCA COPYRIGHT 2004 ACS on STN
- 109:108666 Evidence for specific association between class I major
histocompatibility antigens and the CD8 molecules of human
suppressor/cytotoxic cells. Blue, Marie Luise; Craig, Kimberly A.;
Anderson, Paul; Branton, Kenneth R., Jr.; Schlossman, Stuart F.
(Dana-Farber Cancer Inst., Harvard Med. Sch., Boston, MA, 02115,
USA). Cell (Cambridge, MA, United States), 54(3), 413-21 (English)
1988. CODEN: CELLB5. ISSN: 0092-8674.
- AB Human T lymphocytes, metabolically labeled with 35S-**cysteine**
and 35S-methionine, were reacted with the bifunctional crosslinking
reagent, dithiobis(succinimidylpropionate) (DSP). When detergent
lysates from these cells were immunopptd. with a monoclonal antibody
reactive with the CD8 antigen, a **radiolabeled** protein of
.apprx.44 kd was copptd. with the CD8 mol. Immunoppts. from
detergent lysates prepd. without prior chem. crosslinking contained
only the 33 kd CD8 mol. Similar results were obtained when T
lymphocytes or a cytotoxic T cell clone were **radiolabeled**
with 32P-orthophosphoric acid. The 44 kd CD8-assocd.
protein was **identified** as the heavy chain of the
class I major histocompatibility antigen by depletion in preclearing
expts. with anti-class I MHC antibody and by **peptide**
mapping. The CD8-class I MHC assocn. is due, in part at least, to
disulfide bonding, which may be susceptible to cleavage
during processing of cell lysates.
- CC 15-2 (Immunochemistry)
- IT **Disulfide** group
(of class I histocompatibility antigen-CD8 antigen complexes, of
T-suppressor lymphocyte, of human)

L101 ANSWER 25 OF 28 HCA COPYRIGHT 2004 ACS on STN

109:2641 Human tissue factor contains thioester-linked palmitate and stearate on the cytoplasmic half-cystine. Bach, Ronald; Konigsberg, William H.; Nemerson, Yale (Mt. Sinai Sch. Med., City Univ. New York, New York, NY, 10029, USA). Biochemistry, 27(12), 4227-31 (English) 1988. CODEN: BICHAW. ISSN: 0006-2960.

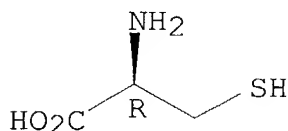
AB The state of the 5 half-cystine residues in human tissue factor (TF) was characterized. The results indicate that the 4 half-cystines in the extracellular domain of TF form 2 **SS** bonds and the half-cystine in the cytoplasmic region is acylated by palmitic acid and stearic acid. The extracellular **SS** crosslinks, Cys49-Cys57 and Cys186-Cys209, were deduced from the anal. of tryptic **peptides**. Acylation of the cytoplasmic half-cystine was demonstrated by purifying and characterizing fibroblast TF from cells labeled with [3H]palmitic acid. **Radiolabeled** fibroblast TF was obsd. by autoradiog. following SDS-PAGE. The tritiated material covalently bound to the **protein** was **identified** as [3H]palmitate and [3H]stearate by reverse-phase HPLC. Deacylation of TF with hydroxylamine resulted in the spontaneous generation of **SS**-linked TF dimers. This suggests that the **SS**-linked TF dimer, a minor component of most TF prepns., and the recently described heterodimeric form of TF are artifacts produced by deacylation of **cysteine**-245 and subsequent interchain **SS** bond formation.

IT 52-90-4P, **Cysteine**, biological studies
(of blood-coagulation factor III, of human, characterization of, **disulfide** formation and thioesterification in relation to)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



CC 6-3 (General Biochemistry)
ST tissue factor **cysteine** palmitate stearate thioester; blood coagulation factor III **cysteine** thioester; **disulfide** group tissue factor
IT **Disulfide** group
(of blood-coagulation factor III, of human)
IT 9035-58-9, Blood-coagulation factor III
(**cysteine** thioesters with palmitate and stearate and

- disulfide groups of, of human)
- IT 52-90-4P, Cysteine, biological studies
(of blood-coagulation factor III, of human, characterization of,
disulfide formation and thioesterification in relation
to)
- L101 ANSWER 26 OF 28 HCA COPYRIGHT 2004 ACS on STN
93:64435 Some physicochemical properties of the deamidase AG from
Pseudomonas fluorescens AG. Rakov, S. S.; Prozorovskii, V. N.;
Grebenshchikova, O. G. (Lab. Enzimol., Moscow, USSR). Probl.
Zlokach. Rosta, 75-80. Editor(s): Berezov, T. T. Univ. Druzhby
Nar. im. Patrisa Lumumby: Moscow, USSR. (Russian) 1977. CODEN:
43RQA4.
- AB The amino acid compn. of deamidase AG (I) from P. fluorescens AG was
detd.; 8 residues of **carboxymethylcysteine** were detected.
I was reduced and carboxymethylated with iodoacetic acid-14C and the
amt. of **radioactivity** in the **protein**
detd. Eight mol. iodoacetate-14C were incorporated/mol I.
Without previous redn. by dithiothreitol, no iodoacetate-14C was
incorporated into I, indicating that the native enzyme contains no
free SH groups. Chymotryptic hydrolysis of carboxymethylated I
resulted in the formation of only 2 **peptides**. Apparently,
I contains 4 **SS** bonds and is composed of no less than 4
subunits. The N-terminal amino acid was lysine; no other N-terminal
amino acids were found. Electrophoresis of I incubated with SDS in
the presence or absence of dithiothreitol or .beta.-mercaptoethanol
resulted in the appearance of 2 protein bands, a major band with
mol. wt. of 30,000 and a 2nd band with mol. w. of 42,000. Thus, I
contains 4 very similar or identical subunits of mol. wt. 30,000.
The subunits of I are not joined by **SS** bonds since I was
dissocd. by SDS alone; it is proposed that each subunit of I
contains 1 **SS** bond. I contains .apprx.9% carbohydrate
which may account for the 2nd band (42,000) obsd. on
electrophoresis.
- CC 7-2 (Enzymes)
- L101 ANSWER 27 OF 28 HCA COPYRIGHT 2004 ACS on STN
83:189816 Subunit structure and amino acid composition of xylose
isomerase from Streptomyces albus. Hogue-Angeletti, Ruth A. (Fox
Chase Cancer Cent., Inst. Cancer Res., Philadelphia, PA, USA).
Journal of Biological Chemistry, 250(19), 7814-18 (English) 1975.
CODEN: JBCHA3. ISSN: 0021-9258.
- AB The subunit structure and amino acid compn. of xylose isomerase from
S. albus were examd. A native mol. wt. of 165,000 detd. by
sedimentation equil. was reduced to 43,000 when the protein was
treated with 6M guanidine-HCl. No further redn. in mol. wt. was
obsd. when potential **SS** bridges of xylose isomerase were
reduced and alkylated, **indicating** that the **protein**

was devoid of interchain **SS** bonds. N-terminal anal. showed 0.86 residues of methionine/41,500 mol. wt. unit. Fractionation of the sol. tryptic **peptides** of S-carboxymethyl xylose isomerase by ion exchange chromatog. and 1-dimensional paper electrophoresis yielded 37-43 **peptides**. When the acid-insol. tryptic **peptides** were dissolved and analyzed by gel filtration techniques, an addnl. 4 **peptides** were found. A unique **radioactive** tryptic **peptide** contg. S-carboxymethylcysteine was found among the sol. **peptides**, confirming **cysteine** as the limiting amino acid residue in the amino acid compn. of xylose isomerase. On the basis of its lysine and arginine content, the no. of tryptic **peptides** is consistent with the hypothesis that the native xylose isomerase is a tetramer of 4 very similar or identical subunits of mol. wt. 41,500, assocd. by noncovalent bonds.

CC 7-5 (Enzymes)

L101 ANSWER 28 OF 28 HCA COPYRIGHT 2004 ACS on STN

57:58717 Original Reference No. 57:11712e-g Significance of **isotope** indicators in development of peculiarities of protein metabolism in organs and tissues in various states of the organism. Konikova, A. S. Tr. Tashkentsk. Konf. po Mirnormu Ispol'z. At. Energii, Akad. Nauk Uz. SSR, 3, 33-7 (Unavailable) 1961.

AB Treatment of myosin with aq. urea to rupture the H bonding of the protein results in a great increase of incorporation of tagged **cysteine**, while the incorporation of methionine is changed but little and incorporation of tyrosine and esp. glycine are greatly decreased. The effect on albumin is similar. Similar results were obtained with in vivo expts. on rabbit serum proteins and liver proteins, with the animals kept in hypothermic state. In such animals the inclusion of glycine and methionine is retarded and that of **cysteine** greatly enhanced. Almost all **cysteine** is bound in this process by strong **peptide** bonds in liver protein, but in serum protein the main bulk of the amino acid is linked by labile **disulfide** bonding. In normally maintained animals the proportion of **disulfide** bonding is only 50%. The changes observed in hypothermia are normalized within 4 days under normal temp. The variability of amino acid incorporation is discussed in the light of possible metabolic cycles.

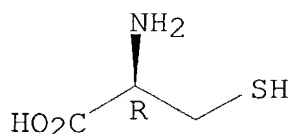
IT 52-90-4, **Cysteine**

(in protein formation, after urea denaturation, H bonding and)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



- CC 69 (Mammalian Physiological Chemistry)
 IT **Isotopes**
 (as indicators, in protein metabolism)
 IT **Peptides**
 (bonds of, **cysteine** binding in proteins of liver by)
 IT **Disulfide** group
 (**cysteine** binding in proteins of blood serum by)
 IT Proteins
 (metabolism of, **isotopes** as indicators of)
 IT **52-90-4, Cysteine** 56-40-6, Glycine 60-18-4,
 Tyrosine
 (in protein formation, after urea denaturation, H bonding and)

=> d 1102 1-24 ti

- L102 ANSWER 1 OF 24 HCA COPYRIGHT 2004 ACS on STN
 TI Characterization of the elusive **disulfide** bridge forming
 human Hb variant:Hb Ta-Li .beta.83 (EF7)Gly.fwdarw.Cys by
 electrospray **mass spectrometry**
- L102 ANSWER 2 OF 24 HCA COPYRIGHT 2004 ACS on STN
 TI Identification of a novel heterodimeric outer membrane protein of
 Porphyromonas gingivalis by two-dimensional gel electrophoresis and
peptide mass fingerprinting
- L102 ANSWER 3 OF 24 HCA COPYRIGHT 2004 ACS on STN
 TI Identification and location of a cysteinyl posttranslational
 modification in an amyloidogenic .kappa.1 light chain protein by
 electrospray ionization and matrix-assisted laser
 desorption/ionization **mass spectrometry**
- L102 ANSWER 4 OF 24 HCA COPYRIGHT 2004 ACS on STN
 TI Determination of **disulfide** bond assignments and
 N-glycosylation sites of the human gastrointestinal carcinoma
 antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM)
- L102 ANSWER 5 OF 24 HCA COPYRIGHT 2004 ACS on STN
 TI Characterization of **cysteine** residues and
disulfide bonds in proteins by liquid
 chromatography/electrospray ionization tandem **mass**
spectrometry

- L102 ANSWER 6 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI **Mass spectrometric** mapping of **disulfide** bonds in recombinant human interleukin-13
- L102 ANSWER 7 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Development of **Disulfide Peptide** Mapping and Determination of **Disulfide** Structure of Recombinant Human Osteoprotegerin Chimera Produced in Escherichia coli
- L102 ANSWER 8 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Albumin Banks Peninsula: a new termination variant characterised by electrospray **mass spectrometry**
- L102 ANSWER 9 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Selective cyanylation of cysteinyl residues as an approach for the **mass spectrometric determination** of **protein** structures
- L102 ANSWER 10 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Selective bridging of bis-cysteinyl residues by arsonous acid derivatives as an approach to the characterization of protein tertiary structures and folding pathways by **mass spectrometry**
- L102 ANSWER 11 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Partial amino acid sequence of .gamma.-46 gliadin
- L102 ANSWER 12 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI **Disulfide** bond assignment in human interleukin-7 by matrix-assisted laser desorption/ionization **mass spectroscopy** and site-directed **cysteine** to serine mutational analysis
- L102 ANSWER 13 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Determination of Tumor Necrosis Factor Binding Protein **Disulfide** Structure: Deviation of the Fourth Domain Structure from the TNFR/NGFR Family **Cysteine**-Rich Region Signature
- L102 ANSWER 14 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Rat liver fatty acid-binding **protein**: **identification** of a molecular species having a mixed **disulfide** with **cysteine** at **cysteine-69** and enhanced protease susceptibility
- L102 ANSWER 15 OF 24 HCA COPYRIGHT 2004 ACS on STN
TI Assignment of protein **disulfides** by a computer method

using mass spectrometric data

L102 ANSWER 16 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI **Disulfide** bonds of herpes simplex virus type 2 glycoprotein gB

L102 ANSWER 17 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI S-Pyridylethylation of intact polyacrylamide gels and in situ **digestion** of electrophoretically separated proteins: a rapid **mass spectrometric** method for identifying **cysteine-containing peptides**

L102 ANSWER 18 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI Cataloguing post-translational modifications of the scrapie prion **protein by mass spectrometry**

L102 ANSWER 19 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI Isolation and characterization of a resistant core **peptide** of recombinant human granulocyte-macrophage colony-stimulating factor (GM-CSF); Confirmation of the GM-CSF amino acid sequence by **mass spectrometry**

L102 ANSWER 20 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI Characterization of a mixture of lobster **digestive cysteine** proteinases by ionspray **mass spectrometry** and tryptic mapping with LC-MS and LC-MS-MS

L102 ANSWER 21 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI **Mass spectrometric** analysis of the structure of .gamma.II bovine lens crystallin

L102 ANSWER 22 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI Strategies for determination of **disulfide** bridges in proteins using plasma desorption **mass spectrometry**

L102 ANSWER 23 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI **Disulfide** bond assignment in human tissue inhibitor of metalloproteinases (TIMP)

L102 ANSWER 24 OF 24 HCA COPYRIGHT 2004 ACS on STN

TI Verification by **mass spectrometry** of the primary structure of human interleukin-2

=> d l102 1,4,5,6,17,22 cbib abs hitstr hitind

L102 ANSWER 1 OF 24 HCA COPYRIGHT 2004 ACS on STN

136:212513 Characterization of the elusive **disulfide** bridge forming human Hb variant:Hb Ta-Li .beta.83 (EF7)Gly.fwdarw.Cys by electrospray **mass spectrometry**. Rai, Dilip K.; Landin, Britta; Griffiths, William J.; Alvelius, Gunvor; Green, Brian N. (Department of Medical Laboratory Sciences and Technology, Division of Clinical Chemistry, Huddinge University Hospital, Karolinska Institutet, Stockholm, Swed.). Journal of the American Society for Mass Spectrometry, 13(2), 187-191 (English) 2002. CODEN: JAMSEF. ISSN: 1044-0305. Publisher: Elsevier Science Inc..

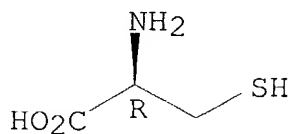
AB An electrospray **mass spectrometric** approach to the identification of a human Hb variant involving a Cys residue incorporation is presented. In Hb Ta-Li (.beta.83Gly .fwdarw. Cys), Cys83 forms intermol. **disulfide** bridges. Routine anal. of the denatured Hb showed the presence of a minor .beta. chain variant whose mass apparently was 1 Da less than the expected mass difference of 46 Da for a Gly .fwdarw. Cys substitution. Redn. of the globin chains with dithiothreitol gave an intense monomer with the expected mass difference for the Gly .fwdarw. Cys substitution. After reprocessing the original raw data from the denatured Hb and taking into account the possibility of dimer formation, a component was revealed whose mass was consistent with a **disulfide** -linked dimer of Ta-Li .beta. globins. The mutation was localized to **peptide** .beta.T10 by anal. of a tryptic **digest**. Tandem **mass spectrometry** and DNA sequencing confirmed the Gly .fwdarw. Cys substitution occurred at residue 83 of the .beta. chain. Problems encountered in identifying the components in mixts. of monomers and dimers are discussed.

IT 52-90-4, L-Cysteine, properties
(electrospray **mass spectrometry** permits characterization of **disulfide** bridge-forming human Hb variant Ta-Li (.beta.83Gly.fwdarw.Cys))

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



CC 6-3 (General Biochemistry)
Section cross-reference(s): 9

ST Hb **cysteine** mutation **disulfide** bridge
mass spectrometry

IT Hemoglobins
(abnormal; electrospray **mass spectrometry**)

- permits characterization of **disulfide** bridge-forming human Hb variant Ta-Li (.beta.83Gly.fwdarw.Cys))
- IT **Disulfide** group
Electrospray ionization **mass spectrometry**
Human
Mutation
(electrospray **mass spectrometry** permits characterization of **disulfide** bridge-forming human Hb variant Ta-Li (.beta.83Gly.fwdarw.Cys))
- IT Quaternary structure
(**protein**; electrospray **mass spectrometry** permits characterization of **disulfide** bridge-forming human Hb variant Ta-Li (.beta.83Gly.fwdarw.Cys))
- IT 52-90-4, L-Cysteine, properties
(electrospray **mass spectrometry** permits characterization of **disulfide** bridge-forming human Hb variant Ta-Li (.beta.83Gly.fwdarw.Cys))

L102 ANSWER 4 OF 24 HCA COPYRIGHT 2004 ACS on STN

- 134:337295 Determination of **disulfide** bond assignments and N-glycosylation sites of the human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM). Chong, Jae Min; Speicher, David W. (Wistar Institute, Philadelphia, PA, 19104, USA). Journal of Biological Chemistry, 276(8), 5804-5813 (English) 2001. CODEN: JBCHA3. ISSN: 0021-9258. Publisher: American Society for Biochemistry and Molecular Biology.
- AB The GA733-2 antigen is a cell surface glycoprotein highly expressed on most human gastrointestinal carcinoma and at a lower level on most normal epithelia. It is an unusual cell-cell adhesion protein that does not exhibit any obvious relation to the four known classes of adhesion mols. In this study, the **disulfide**-bonding pattern of the GA733-2 antigen was detd. using matrix-assisted laser desorption/ionization **mass spectrometry** and N-terminal sequencing of purified tryptic **peptides** treated with 2-[2'-nitrophenylsulfonyl]-3-methyl-3-bromoindolenine or partially reduced and alkylated. Numbering GA733-2 **cysteines** sequentially from the N terminus, the first three **disulfide** linkages are Cys1-Cys4, Cys2-Cys6, and Cys3-Cys5, which is a novel pattern for a **cysteine**-rich domain instead of the expected epidermal growth factor-like **disulfide** structure. The next three **disulfide** linkages are Cys7-Cys8, Cys9-Cys10, and Cys11-Cys12, consistent with the recently detd. **disulfide** pattern of the thyroglobulin type 1A domain of insulin-like growth factor-binding proteins 1 and 6. Anal. of glycosylation sites showed that GA733-2 antigen contained N-linked carbohydrate but that no O-linked carbohydrate groups were detected. Of the three potential N-linked glycosylation

sites, Asn175 was not glycosylated, whereas Asn88 was completely glycosylated, and Asn51 was partially glycosylated. Thus, the extracellular domain of the GA733-2 antigen consists of three distinct domains; a novel **cysteine**-rich N-terminal domain (GA733 type 1 motif), a **cysteine**-rich thyroglobulin type 1A domain (GA733 type 2 motif), and a unique nonglycosylated domain without **cysteines** (GA733 type 3 motif).

- CC 6-3 (General Biochemistry)
Section cross-reference(s): 14
- ST gastrointestinal carcinoma antigen GA733 2 **disulfide** bond glycosylation site
- IT Antigens
(17-1A; detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Cell adhesion molecules
(Ep-CAM as; detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Digestive tract
(carcinoma; detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Protein motifs
(**cysteine**-rich N-terminal domain; detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Protein motifs
(**cysteine**-rich thyroglobulin type 1A domain; detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Disulfide group
(detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Protein motifs
(glycosylation site; detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Conformation
(loop, **protein**; detn. of **disulfide** bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))
- IT Protein motifs
(nonglycosylated domain without **cysteines**; detn. of

disulfide bond assignments and N-glycosylation sites of human gastrointestinal carcinoma antigen GA733-2 (CO17-1A, EGP, KS1-4, KSA, and Ep-CAM))

L102 ANSWER 5 OF 24 HCA COPYRIGHT 2004 ACS on STN

133:346639 Characterization of **cysteine** residues and

disulfide bonds in proteins by liquid

chromatography/electrospray ionization tandem **mass**

spectrometry. Yen, Ten-Yang; Joshi, Rajesh K.; Yan, Hui;

Seto, Nina O. L.; Palcic, Monica M.; Macher, Bruce A. (Department of Chemistry and Biochemistry, San Francisco State University, San Francisco, CA, 94132, USA). Journal of Mass Spectrometry, 35(8), 990-1002 (English) 2000. CODEN: JMSPFJ. ISSN: 1076-5174.

Publisher: John Wiley & Sons Ltd..

AB **Cysteine** residues and **disulfide** bonds are important for protein structure and function. We have developed a simple and sensitive method for detg. the presence of free **cysteine** (Cys) residues and **disulfide** bonded Cys residues in proteins (<100 pmol) by liq. chromatog./electrospray ionization tandem **mass spectrometry** (LC/ESI-MS/MS) in combination with protein database searching using the program Sequest. Free Cys residues in a protein were labeled with PEO-maleimide biotin immediately followed by denaturation with 8 M urea. Subsequently, the protein was **digested** with trypsin or chymotrypsin and the resulting products were analyzed by capillary LC/ESI-MS/MS for **peptides** contg. modified Cys and/or **disulfide** bonded Cys residues. Although the **MS** method for identifying **disulfide** bonds has been routinely employed, methods to prevent thiol-**disulfide** exchange have not been well documented. Our protocol was found to minimize the occurrence of the thiol-**disulfide** exchange reaction. The method was validated using well-characterized proteins such as aldolase, ovalbumin, and .beta.-lactoglobulin A. We also applied this method to characterize Cys residues and **disulfide** bonds of .beta. 1,4-galactosyltransferase (five Cys), and human blood group A and B glycosyltransferases (four Cys). Our results demonstrate that .beta. 1,4-galactosyltransferase contains one free Cys residue and two **disulfide** bonds, which is in contrast to work previously reported using chem. methods for the characterization of free Cys residues, but is consistent with recently published results from x-ray crystallog. In contrast to the results obtained for .beta. 1,4-galactosyltransferase, none of the Cys residues in A and B glycosyltransferases were found to be involved in **disulfide** bonds.

IT 52-90-4, **Cysteine**, analysis

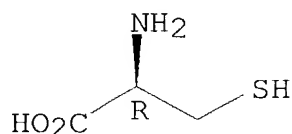
(characterization of **cysteine** residues and **disulfide** bonds in proteins by liq.

chromatog./electrospray ionization tandem **mass spectrometry**)

RN 52-90-4 HCA

CN L-Cysteine (9CI) (CA INDEX NAME)

Absolute stereochemistry.



CC 9-5 (Biochemical Methods)

Section cross-reference(s): 6, 7

ST **cysteine disulfide** bond protein electrospray ionization **mass spectrometry**

IT **Digestion**, chemical

Disulfide group

Electrospray ionization **mass spectrometry**

Sample preparation

pH

(characterization of **cysteine** residues and **disulfide** bonds in proteins by liq.

chromatog./electrospray ionization tandem **mass spectrometry**)

IT **Proteins**, general, analysis

(characterization of **cysteine** residues and **disulfide** bonds in proteins by liq.

chromatog./electrospray ionization tandem **mass spectrometry**)

IT Ovalbumin

(characterization of **cysteine** residues and **disulfide** bonds in proteins by liq.

chromatog./electrospray ionization tandem **mass spectrometry**)

IT Liquid chromatography

(coupled with electrospray ionization tandem **mass spectrometry**; characterization of **cysteine**

residues and **disulfide** bonds in proteins by liq.

chromatog./electrospray ionization tandem **mass spectrometry**)

IT **Mass spectrometry**

Mass spectrometry

(liq. chromatog. combined with; characterization of **cysteine** residues and **disulfide** bonds in

proteins by liq. chromatog./electrospray ionization tandem **mass spectrometry**)

- IT Liquid chromatography
Liquid chromatography
(**mass spectrometry** combined with;
characterization of **cysteine** residues and
disulfide bonds in proteins by liq.
chromatog./electrospray ionization tandem **mass**
spectrometry)
- IT Conformation
Denaturation
(protein; characterization of **cysteine** residues and
disulfide bonds in proteins by liq.
chromatog./electrospray ionization tandem **mass**
spectrometry)
- IT Information systems
(searching, computer database; characterization of
cysteine residues and **disulfide** bonds in
proteins by liq. chromatog./electrospray ionization tandem
mass spectrometry)
- IT Lactoglobulins
(.beta.-, A; characterization of **cysteine** residues and
disulfide bonds in proteins by liq.
chromatog./electrospray ionization tandem **mass**
spectrometry)
- IT 52-90-4, **Cysteine**, analysis 9024-52-6, Aldolase
9067-69-0, A-Antigen-forming acetylgalactosaminyltransferase
37257-33-3, Blood group B glycosyltransferase
(characterization of **cysteine** residues and
disulfide bonds in proteins by liq.
chromatog./electrospray ionization tandem **mass**
spectrometry)
- IT 93285-75-7 305372-39-8
(characterization of **cysteine** residues and
disulfide bonds in proteins by liq.
chromatog./electrospray ionization tandem **mass**
spectrometry)
- IT 9054-94-8
(characterization of **cysteine** residues and
disulfide bonds in proteins by liq.
chromatog./electrospray ionization tandem **mass**
spectrometry)

L102 ANSWER 6 OF 24 HCA COPYRIGHT 2004 ACS on STN

133:3553 **Mass spectrometric** mapping of

disulfide bonds in recombinant human interleukin-13.

Tsarbopoulos, Anthony; Varnerin, Jeff; Cannon-Carlson, Susan; Wylie, David; Pramanik, Birendra; Tang, John; Nagabhushan, Tattanahalli L.
(Departments of Bioisolation Process Development and Production,
Schering-Plough Research Institute, Union, NJ, 07083, USA). Journal

- of Mass Spectrometry, 35(3), 446-453 (English) 2000. CODEN: JMSPFJ. ISSN: 1076-5174. Publisher: John Wiley & Sons Ltd..
- AB Interleukin 13 (IL-13), a member of the .alpha.-helical family of cytokines, has .apprx.30% primary sequence homol. with IL-4 and shares a common receptor component. The biol. active rhIL-13 is monomeric and non-glycosylated, and contains two **disulfide** bonds as detd. by comparative electrospray **mass spectrometric (MS)** anal. of the **protein** before and after redn. with dithiothreitol-dithioerythritol. A trypsin-resistant core **peptide** of rhIL-13 was isolated and analyzed by plasma desorption (PD) **MS**, identifying a **disulfide**-linked core **peptide**. Subsequent **digestion** of this core **peptide** by pepsin, followed by PDMS anal. of the resulting cystine-contg. peptic fragments, provided rapid detn. of the existing **disulfide** bonds between **cysteine** residues 28-56 and 44-70. This **disulfide** arrangement is similar to that obsd. for the analogous four internal **cysteine** residues in hIL-4. The conservation of **disulfide** bond arrangements between hIL-13 and hIL-4, coupled with their .alpha.-helical structure and sequence homologies, confirms that IL-13 and IL-4 are structural homologs. It is also consistent with their reported similarities in biol. function and receptor binding kinetics.
- CC 15-5 (Immunochemistry)
- ST **disulfide** bond interleukin 13
- IT Interleukin 13
(**disulfide** linkage assignment in recombinant human IL-13)
- IT **Disulfide** group
(linkage assignment in recombinant human interleukin-13)
- L102 ANSWER 17 OF 24 HCA COPYRIGHT 2004 ACS on STN
- 125:81167 S-Pyridylethylation of intact polyacrylamide gels and in situ **digestion** of electrophoretically separated proteins: a rapid **mass spectrometric** method for identifying **cysteine**-containing **peptides**. Moritz, Robert L.; Eddes, James S.; Reid, Gavin E.; Simpson, Richard J. (Ludwig Inst. Cancer Res., Walter Eliza Hall Inst. Med. Res., Parkville, Australia). Electrophoresis, 17(5), 907-917 (English) 1996. CODEN: ELCTDN. ISSN: 0173-0835. Publisher: VCH.
- AB In-gel proteolytic **digestion** of acrylamide-gel sepd. proteins is a method widely used for generating **peptide** fragments for the purpose of **identifying proteins** by Edman degrdn., tandem **mass spectrometry**, and **peptide-mass** fingerprinting. However, it is well recognized for **disulfide**-bonded proteins electrophoresed under reducing conditions that if no precautions are taken to

minimize **disulfide** bond formation during protein **digestion** or **peptide** isolation, complex **peptide** maps can result. Here, we describe an improved method for in-gel protein **digestion**. It consists of first reducing and S-pyridylethylating Coomassie Brilliant Blue R-250-stained proteins immobilized in the whole-gel slab with dithiothreitol and 4-vinylpyridine, excising the individual stained and alkylated proteins, and then **digesting** them in situ in the gel matrix with trypsin or *Achromobacter lyticus* protease I. **Peptide** fragments generated in this manner are extd. from the gel piece and purified to homogeneity by a rapid (.1 to req. 12 min) reversed-phase high performance liq. chromatog. (HPLC) procedure, based upon conventional silica supports. Recoveries of **peptides** are increased by S-pyridylethylation of acrylamide-immobilized proteins prior to in-gel **digestion**. Further, the levels of gel-related contaminants, which otherwise result in suppression of sample signals during electrospray ionization **mass spectrometry**, are greatly reduced by the redn./alkylation step. Addnl., we demonstrate the S-.beta.-(4-pyridylethyl)-**cysteine** contg. **peptides** can be readily identified during reversed-phase HPLC by absorbance at 254 nm, and during electrospray ionization tandem **mass spectrometry** by the appearance of a characteristic-pyridylethyl fragment ion of 106 Da. The position of **cysteine** residues in a sequence can be detd. as phenylthiohydantoin S-.beta.-(4-pyridylethyl)-**cysteine** during Edman degradn., and by tandem **mass spectrometry**.

CC 9-16 (Biochemical Methods)

ST pyridylethylation polyacrylamide gel **digestion**
electrophoresis; **protein mass spectrometry cysteine peptide**

IT Edman degradation
(S-Pyridylethylation of intact polyacrylamide gels and in situ **digestion** of electrophoretically sepd. proteins: a rapid **mass spectrometric** method for identifying **cysteine-contg. peptides**)

IT **Peptides, analysis**
(**cysteine-contg.**, S-Pyridylethylation of intact polyacrylamide gels and in situ **digestion** of electrophoretically sepd. proteins: a rapid **mass spectrometric** method for identifying **cysteine-contg. peptides**)

IT **Mass spectrometry**
(tandem, S-Pyridylethylation of intact polyacrylamide gels and in situ **digestion** of electrophoretically sepd. proteins: a rapid **mass spectrometric** method for identifying **cysteine-contg. peptides**)

- IT 100-43-6, 4-Vinylpyridine 3483-12-3, Dithiothreitol
(S-Pyridylethylation of intact polyacrylamide gels and in situ
digestion of electrophoretically sepd. proteins: a rapid
mass spectrometric method for identifying
cysteine-contg. **peptides**)
- L102 ANSWER 22 OF 24 HCA COPYRIGHT 2004 ACS on STN
114:58326 Strategies for determination of **disulfide** bridges in
proteins using plasma desorption **mass spectrometry**
. Soerensen, Hans Holmegaard; Thomsen, Johannes; Bayne, Stephen;
Hoejrup, Peter; Roepstorff, Peter (Novo Nordisk A/S, Gentofte,
DK-2820, Den.). Biomedical & Environmental Mass Spectrometry,
19(11), 713-20 (English) 1990. CODEN: BEMSEN. ISSN: 0887-6134.
- AB **Disulfide** bridges have been assigned in 3 different
proteins by locating possible **disulfide**-linked
peptides in enzymic **digests** of the proteins based
on their mol. wt. detd. by plasma desorption **mass**
spectrometry. Different strategies have been employed
including in situ redn. of the nitrocellulose-bound **peptides**
and confirmation of **peptide** identify by Me esterification
reactions or Edman degrdn. The latter was needed for identification
of glycosylated **disulfide**-linked **peptides**. For
insulins cleaved between **cysteine** residues in close
proximity was not possible; but a combination of mol. mass
information, enzymic cleavage with 2 different enzymes and sequence
anal. including identification of diphenylthiohydantoin-cystine
could ensure an unambiguous assignment of the **disulfide**
bridges.
- CC 9-5 (Biochemical Methods)
Section cross-reference(s): 6
- ST **disulfide** group detn protein
mass spectrometry; plasma desorption **mass**
spectrometry protein **disulfide**
- IT **Disulfide** group
(detn. of, in **proteins** by plasma desorption
mass spectrometry, strategies for)
- IT Glycoproteins, analysis
(**disulfide** bridges detn. in, by plasma desorption
mass spectrometry, strategies for)
- IT Proteins, specific or class
(15,000-mol.-wt., **disulfide** bridges detn. in, by plasma
desorption **mass spectrometry**, strategies for)
- IT Proteins, specific or class
(**disulfide**-contg., **disulfide** bridges detn.
in, by plasma desorption **mass spectrometry**,
strategies for)
- IT **Mass spectroscopy**
(plasma-desorption, **disulfide** bridges in